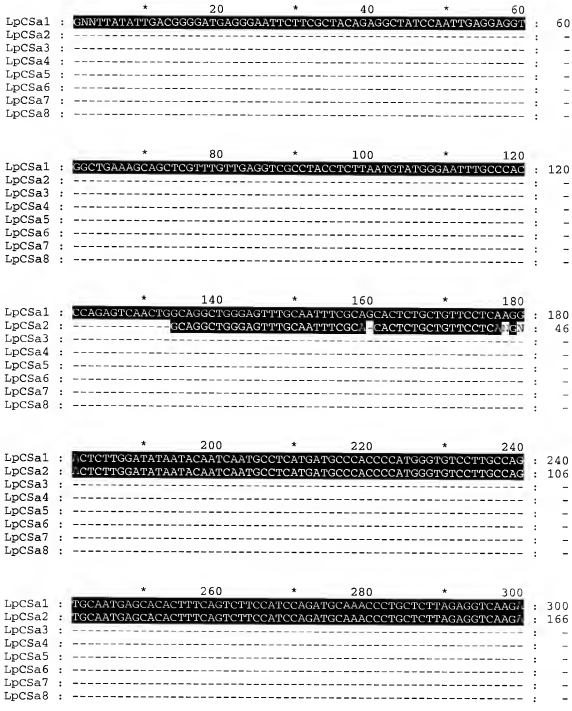
LpCSa1 : GNNTTATATTGACGGGGATGAGGGAATTCTTCGCTACAGAGGCTATCCAATTGAGGAGGT : 60
LpCSa2 : ---------- : -
LpCSa3 : ---------- : -
LpCSa4 : ---------- : -
LpCSa5 : ---------- : -
LpCSa6 : ---------- : -
LpCSa7 : ---------- : -
LpCSa8 : ---------- : -
LpCSa1 : GGCTGAAAGCAGCTCGTTTGTTGAGGTCGCCTACCTCTTAATGTATGGGAATTTGCCCAC : 120
LpCSa2 : ---------- : -
LpCSa3 : ---------- : -
LpCSa4 : ---------- : -
LpCSa5 : ---------- : -
LpCSa6 : ---------- : -
LpCSa7 : ---------- : -
LpCSa8 : ---------- : -
LpCSa1 : CCAGAGTCAACTGGCAGGCTGGGAGTTTGCAATTTCGCAGCACTCTGCTGTTCCTCAAGG : 180
LpCSa2 : ----------GCAGGCTGGGAGTTTGCAATTTCGCA-CACTCTGCTGTTCCTCA-GN : 46
LpCSa3 : ---------- : -
LpCSa4 : ---------- : -
LpCSa5 : ---------- : -
LpCSa6 : ---------- : -
LpCSa7 : ---------- : -
LpCSa8 : ---------- : -
LpCSa1 : ACTCTTGGATATAATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAG : 240
LpCSa2 : ACTCTTGGATATAATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAG : 106
LpCSa3 : ---------- : -
LpCSa4 : ---------- : -
LpCSa5 : ---------- : -
LpCSa6 : ---------- : -
LpCSa7 : ---------- : -
LpCSa8 : ---------- : -
LpCSa1 : TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA : 300
LpCSa2 : TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA : 166
LpCSa3 : ---------- : -
LpCSa4 : ---------- : -
LpCSa5 : ---------- : -
LpCSa6 : ---------- : -
LpCSa7 : ---------- : -
LpCSa8 : ---------- : -

**FIGURE 1**

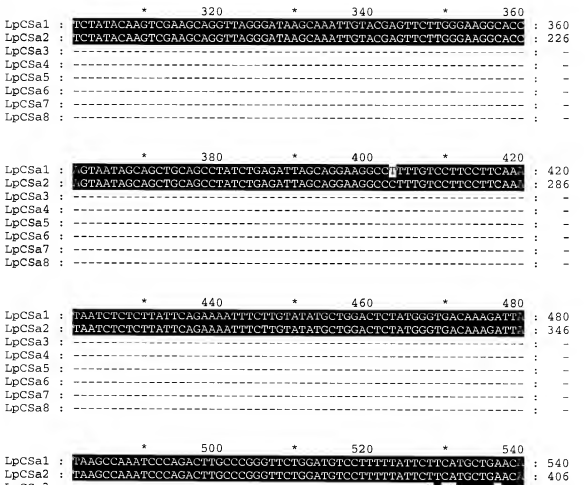


**FIGURE 1 (cont.)**

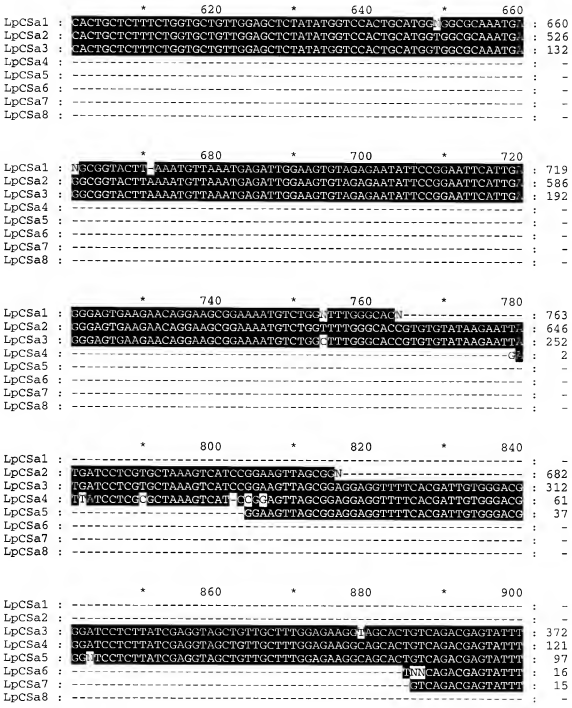


**FIGURE 1 (cont.)**

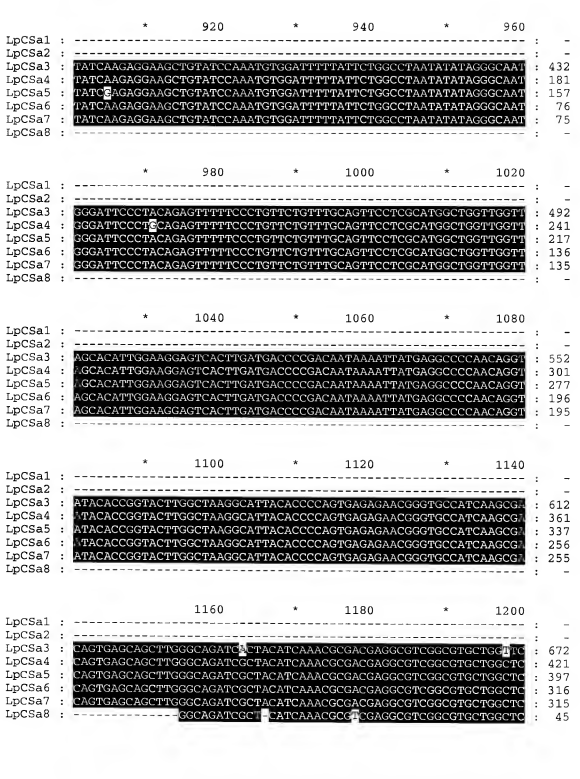


**FIGURE 1 (cont.)**

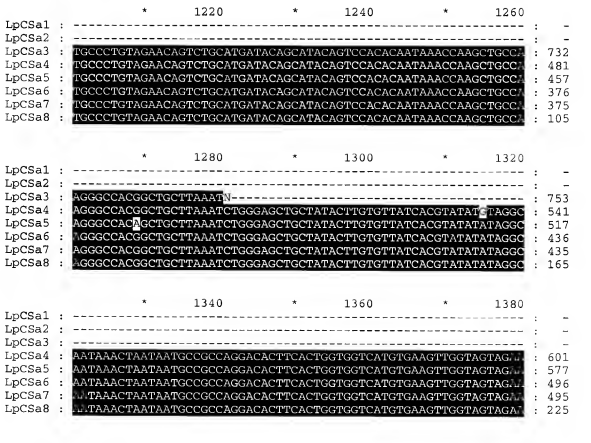


**FIGURE 1 (cont.)**

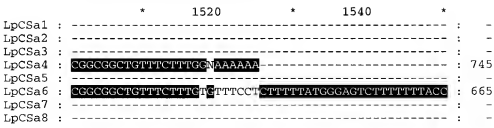


**FIGURE 1 (cont.)**

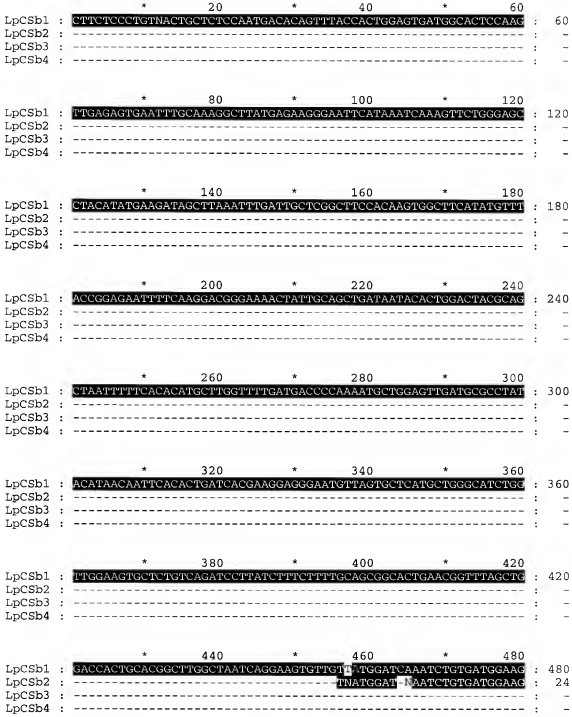
LpCSb1 : CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTTACCACTGGAGTGATGGCACTCCAAG : 60
LpCSb2 : ---------- : -
LpCSb3 : ---------- : -
LpCSb4 : ---------- : -
LpCSb1 : TTGAGAGTGAATTTGCAAAGGCTTATGAGAAGGGAATTCATAAATCAAAGTTCTGGGAGC : 120
LpCSb2 : ---------- : -
LpCSb3 : ---------- : -
LpCSb4 : ---------- : -
LpCSb1 : CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT : 180
LpCSb2 : ---------- : -
LpCSb3 : ---------- : -
LpCSb4 : ---------- : -
LpCSb1 : ACCGGAGAATTTTCAAGGACGGGAAAACTATTGCAGCTGATAATACACTGGACTACGCAG : 240
LpCSb2 : ---------- : -
LpCSb3 : ---------- : -
LpCSb4 : ---------- : -
LpCSb1 : CTAATTTTTCACACATGCTTGGTTTTGATGACCCCAAAATGCTGGAGTTGATGCGCCTAT : 300
LpCSb2 : ---------- : -
LpCSb3 : ---------- : -
LpCSb4 : ---------- : -
LpCSb1 : ACATAACAATTCACACTGATCACGAAGGAGGGAATGTTAGTGCTCATGCTGGGCATCTGG : 360
LpCSb2 : ---------- : -
LpCSb3 : ---------- : -
LpCSb4 : ---------- : -
LpCSb1 : TTGGAAGTGCTCTGTCAGATCCTTATCTTTCTTTTGCAGCGGCACTGAACGGTTTAGCTG : 420
LpCSb2 : ---------- : -
LpCSb3 : ---------- : -
LpCSb4 : ---------- : -
LpCSb1 : GACCACTGCACGGCTTGGCTAATCAGGAAGTGTTGTTCTGGATCAAATCTGTGATGGAAG : 480
LpCSb2 : ----------TNATGGAT-NAATCTGTGATGGAAG : 24
LpCSb3 : ---------- : -
LpCSb4 : ---------- : -

FIGURE 2

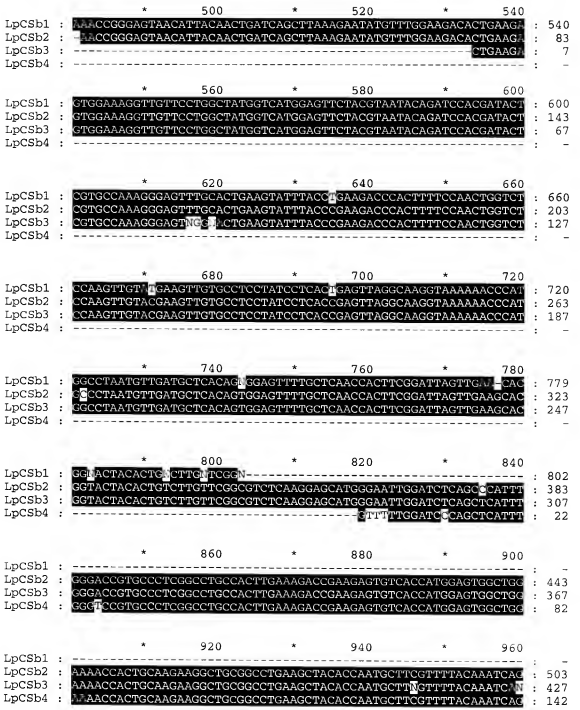


**FIGURE 2 (cont.)**

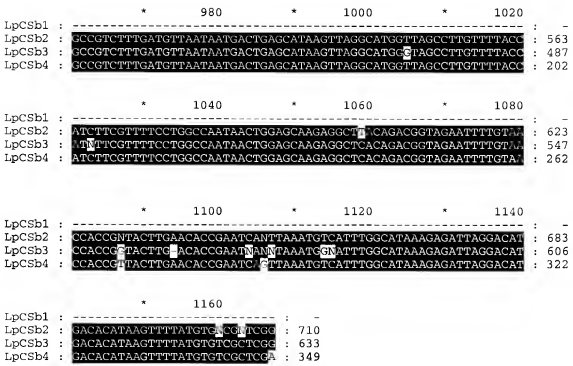


**FIGURE 2 (cont.)**

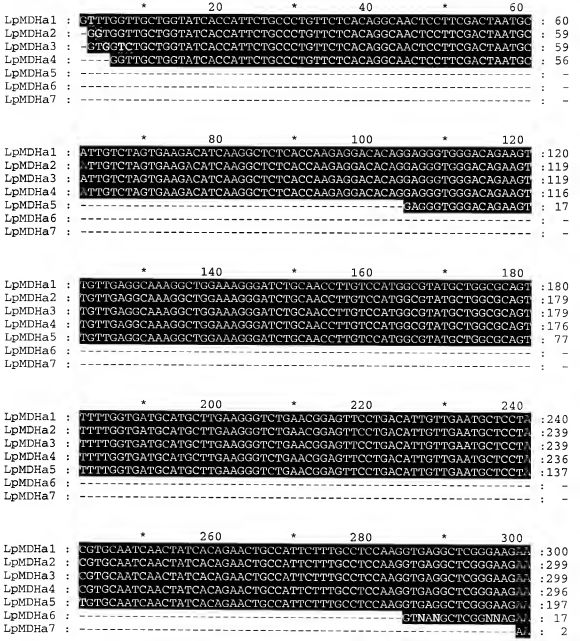
LpMDHa1 : GTTTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC : 60
LpMDHa2 : -GGTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC : 59
LpMDHa3 : -GTGGTCTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC : 59
LpMDHa4 : ----GGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC : 56
LpMDHa5 : ---------- : -
LpMDHa6 : ---------- : -
LpMDHa7 : ---------- : -
LpMDHa1 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT :120
LpMDHa2 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT :119
LpMDHa3 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT :119
LpMDHa4 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT :116
LpMDHa5 : ----------GAGGGTGGGACAGAAGT : 17
LpMDHa6 : ---------- : -
LpMDHa7 : ---------- : -
LpMDHa1 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT :180
LpMDHa2 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT :179
LpMDHa3 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT :179
LpMDHa4 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT :176
LpMDHa5 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 77
LpMDHa6 : ---------- : -
LpMDHa7 : ---------- : -
LpMDHa1 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA :240
LpMDHa2 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA :239
LpMDHa3 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA :239
LpMDHa4 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA :236
LpMDHa5 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA :137
LpMDHa6 : ---------- : -
LpMDHa7 : ---------- : -
LpMDHa1 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA :300
LpMDHa2 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA :299
LpMDHa3 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA :299
LpMDHa4 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA :296
LpMDHa5 : TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA :197
LpMDHa6 : ----------GTNANGCTCGGNNAGAA : 17
LpMDHa7 : ----------AA : 2

FIGURE 3

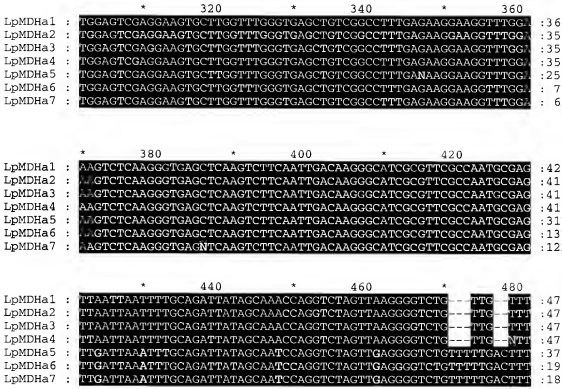


**FIGURE 3 (cont.)**

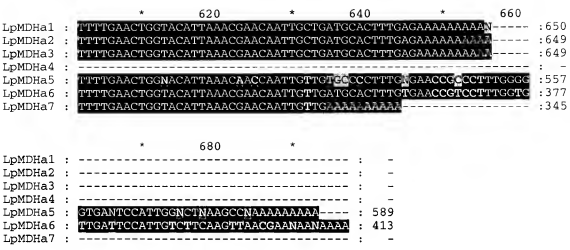


**FIGURE 3 (cont.)**

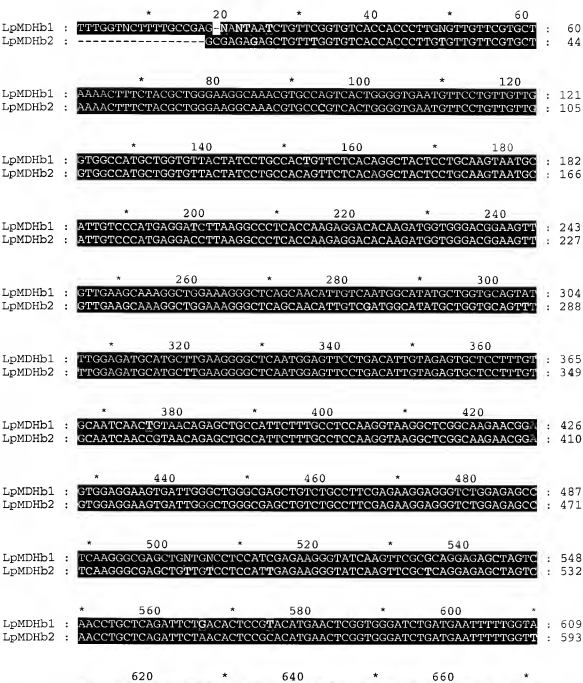
LpMDHb1 : TTTGGTNCTTTTGCCGAG-NANTAATCTGTTCGGTGTCACCACCCTTGNGTTGTTCGTGCT : 60
LpMDHb2 : ----------GCGAGAGAGCTGTTTGGTGTCACCACCCTTGTGTTGTTCGTGCT : 44
LpMDHb1 : AAAACTTTCTACGCTGGGAAGGCAAACGTGCCAGTCACTGGGGTGAATGTTCCTGTTGTTC : 121
LpMDHb2 : AAAACTTTCTACGCTGGGAAGGCAAACGTGCCCGTCACTGGGGTGAATGTTCCTGTTGTTC : 105
LpMDHb1 : GTGGCCATGCTGGTGTTACTATCCTGCCACTGTTCTCACAGGCTACTCCTGCAAGTAATGC : 182
LpMDHb2 : GTGGCCATGCTGGTGTTACTATCCTGCCACAGTTCTCACAGGCTACTCCTGCAAGTAATGC : 166
LpMDHb1 : ATTGTCCCATGAGGATCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT : 243
LpMDHb2 : ATTGTCCCATGAGGACCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT : 227
LpMDHb1 : GTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCAATGGCATATGCTGGTGCAGTAT : 304
LpMDHb2 : GTTGAAGCAAAGGCTGGAAAGGCTCAGCAACATTGTCGATGGCATATGCTGGTGCAGTTT : 288
LpMDHb1 : TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT : 365
LpMDHb2 : TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT : 349
LpMDHb1 : GCAATCAACTGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA : 426
LpMDHb2 : GCAATCAACCGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA : 410
LpMDHb1 : GTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCTGGAGAGCC : 487
LpMDHb2 : GTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCTGGAGAGCC : 471
LpMDHb1 : TCAAGGGCGAGCTGNTGNCCTCCATCGAGAAGGGTATCAAGTTCGCGCAGGAGAGCTAGTC : 548
LpMDHb2 : TCAAGGGCGAGCTGTTGTCCTCCATTGAGAAGGGTATCAAGTTCGCTCAGGAGAGCTAGTC : 532
LpMDHb1 : AACCTGCTCAGATTCTGACACTCCGTACATGAACTCGGTGGGATCTGATGAATTTTTGGTA : 609
LpMDHb2 : AACCTGCTCAGATTCTAACACTCCGCACATGAACTCGGTGGGATCTGATGAATTTTTGGTT : 593
LpMDHb1 : CGACTCCTTTCTCTGCCCCTTTTTCGTGGGGACATTGAGGCGTTGNGCTTCACATTAAAAT : 670
LpMDHb2 : CGACTCCTTTCACTGCCCCCTTCTCCTGGGGACATTGAGGCGTCGTGCTCCACAATAAAAT : 654

FIGURE 4

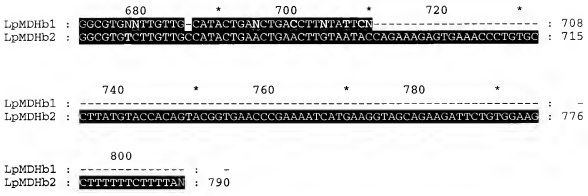


**FIGURE 4 (cont.)**

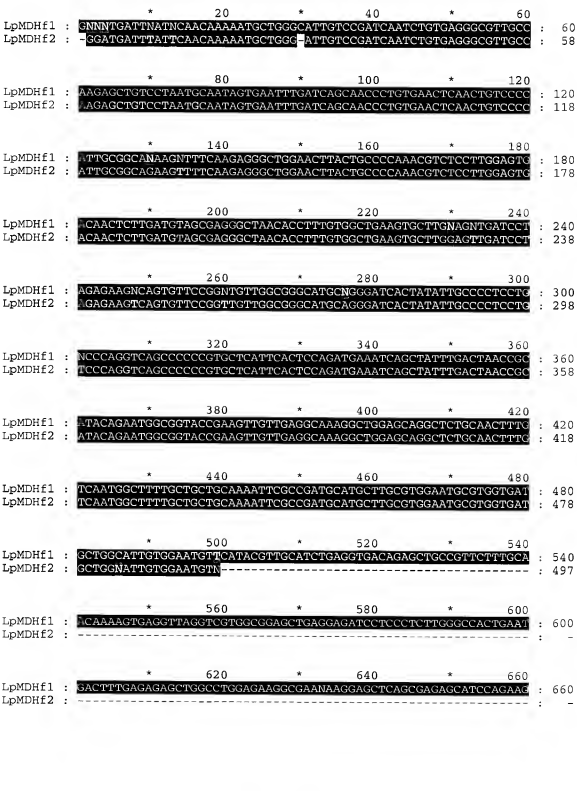
LpMDHf1 : GNNNTGATTNATNCAACAAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC : 60
LpMDHf2 : -GGATGATTTATTCAACAAAAATGCTGGG-ATTGTCCGATCAATCTGTGAGGGCGTTGCC : 58
LpMDHf1 : AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 120
LpMDHf2 : AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 118
LpMDHf1 : ATTGCGGCANAAGNTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG : 180
LpMDHf2 : ATTGCGGCAGAAGTTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG : 178
LpMDHf1 : ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGNAGNTGATCCT : 240
LpMDHf2 : ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGGAGTTGATCCT : 238
LpMDHf1 : AGAGAAGNCAGTGTTCCGGNTGTTGGCGGGCATGCNGGGATCACTATATTGCCCCTCCTG : 300
LpMDHf2 : AGAGAAGTCAGTGTTCCGGTTGTTGGCGGGCATGCAGGGATCACTATATTGCCCCTCCTG : 298
LpMDHf1 : NCCCAGGTCAGCCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC : 360
LpMDHf2 : TCCCAGGTCAGCCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC : 358
LpMDHf1 : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTC : 420
LpMDHf2 : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTC : 418
LpMDHf1 : TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT : 480
LpMDHf2 : TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT : 478
LpMDHf1 : GCTGGCATTGTGGAATGTTCATACGTTGCATCTGAGGTGACAGAGGTGCCGTTCTTTGCA : 540
LpMDHf2 : GCTGGNATTGTGGAATGTN---------- : 497
LpMDHf1 : NCAAAAGTGAGGTTAGGTCGTGGCGGAGCTGAGGAGATCCTCCCTCTTGGGCCACTGAAT : 600
LpMDHf2 : ---------- : -
LpMDHf1 : GACTTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAGGAGCTCAGCGAGAGCATCCAGAAE : 660
LpMDHf2 : ---------- : -

FIGURE 5

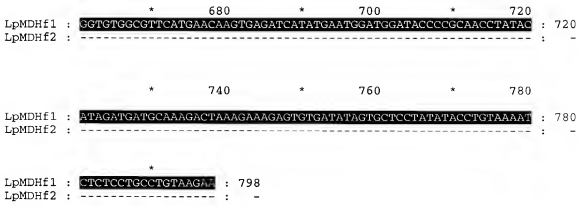


**FIGURE 5 (cont.)**

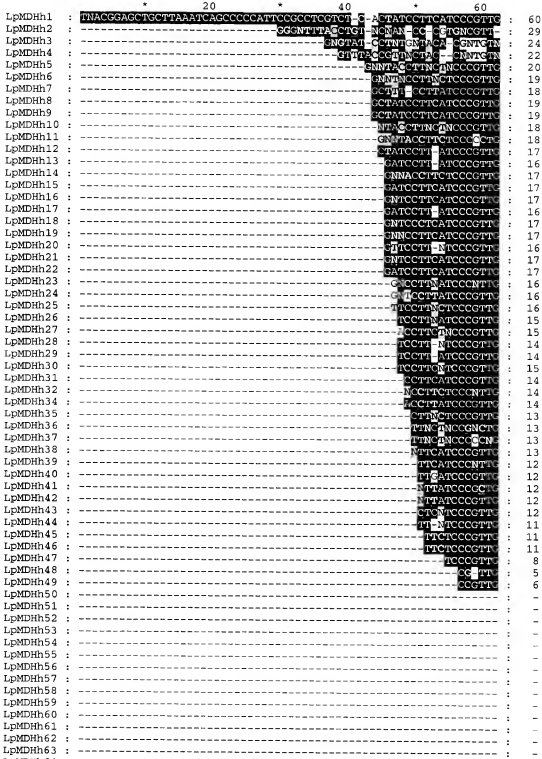

FIGURE 6

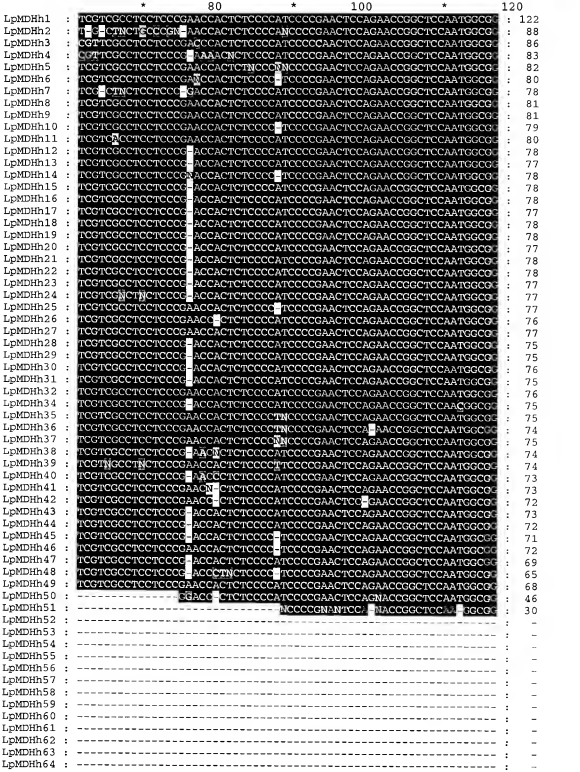

FIGURE 6 (cont)

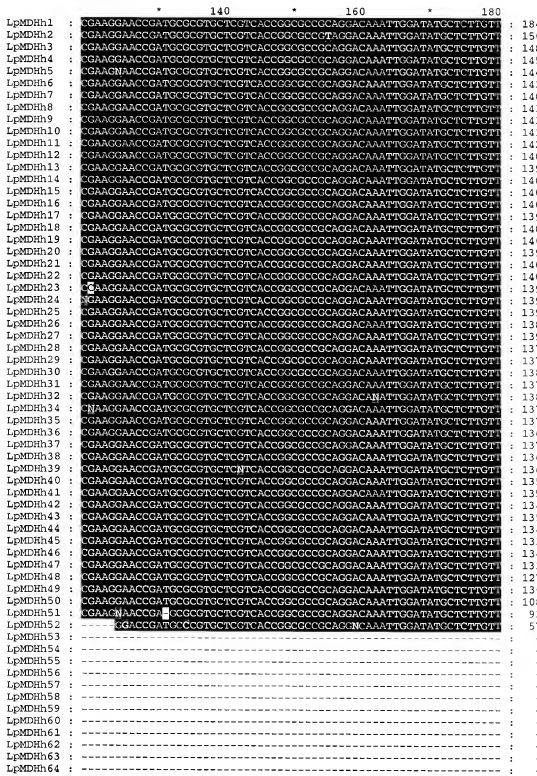


**FIGURE 6 (cont.)**


**FIGURE 6 (cont.)**

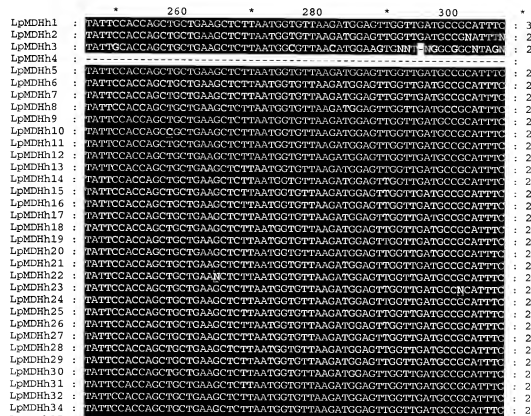


**FIGURE 6 (cont.)**

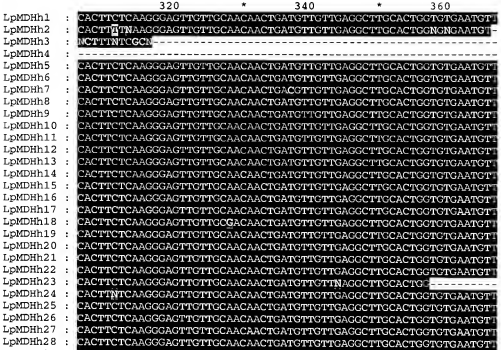


**FIGURE 6 (cont.)**


**FIGURE 6 (cont.)**

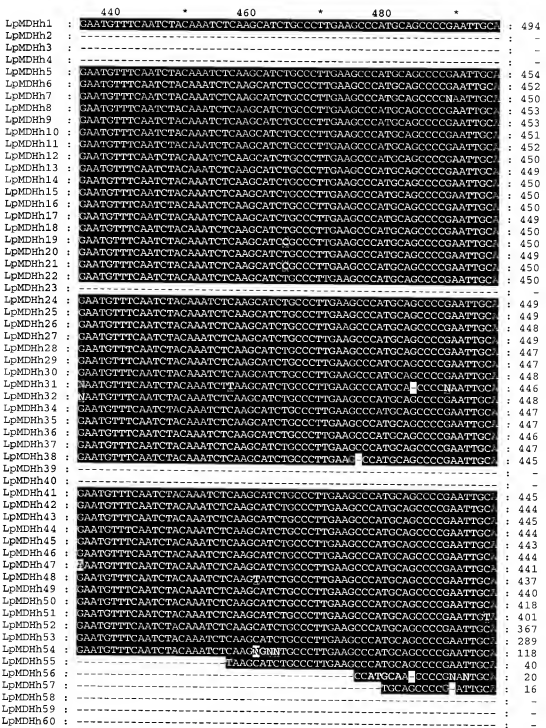


**FIGURE 6 (cont.)**

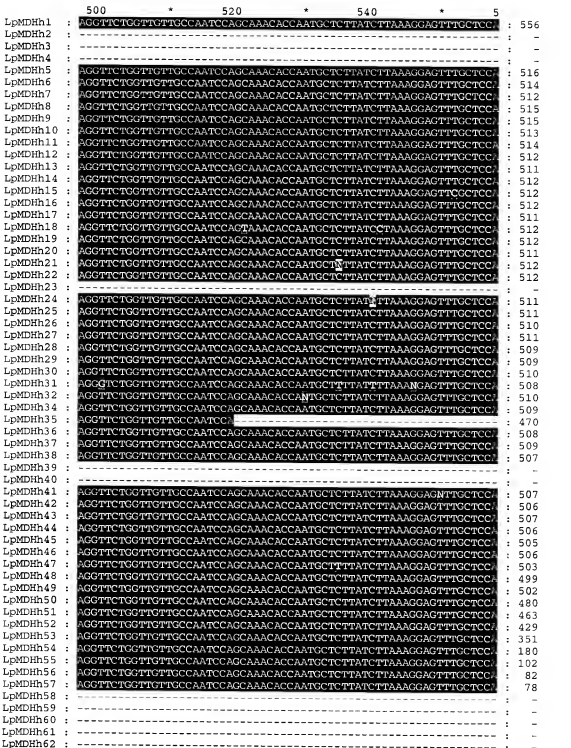


**FIGURE 6 (cont.)**

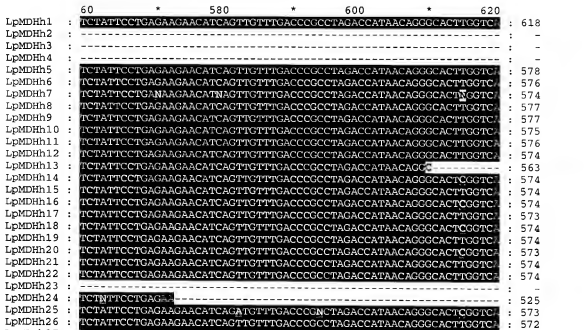


**FIGURE 6 (cont.)**

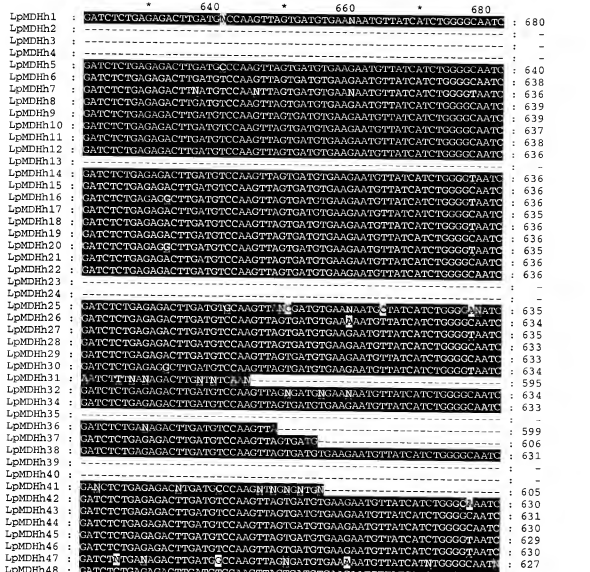


**FIGURE 6 (cont.)**

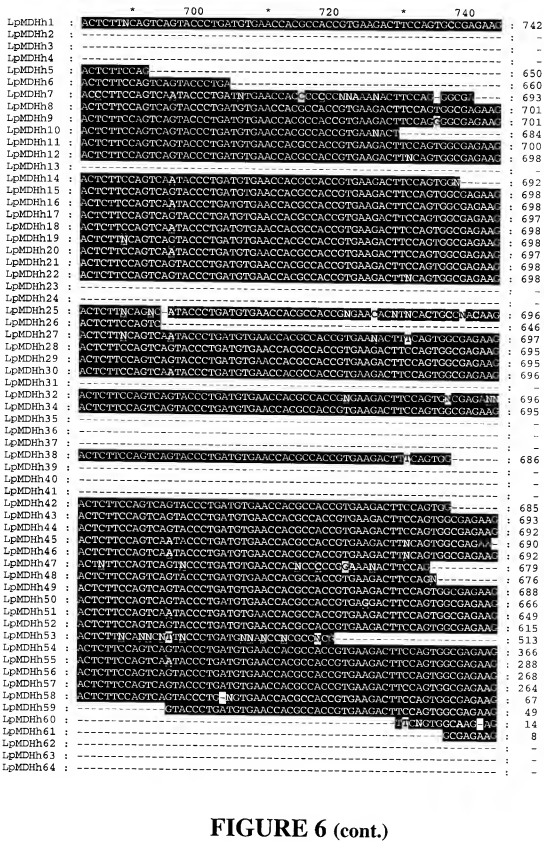

FIGURE 6 (cont.)

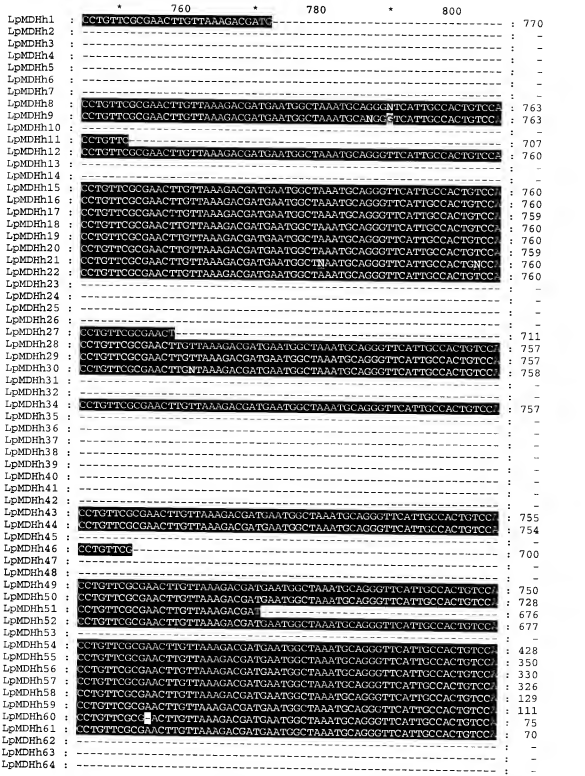


**FIGURE 6 (cont.)**

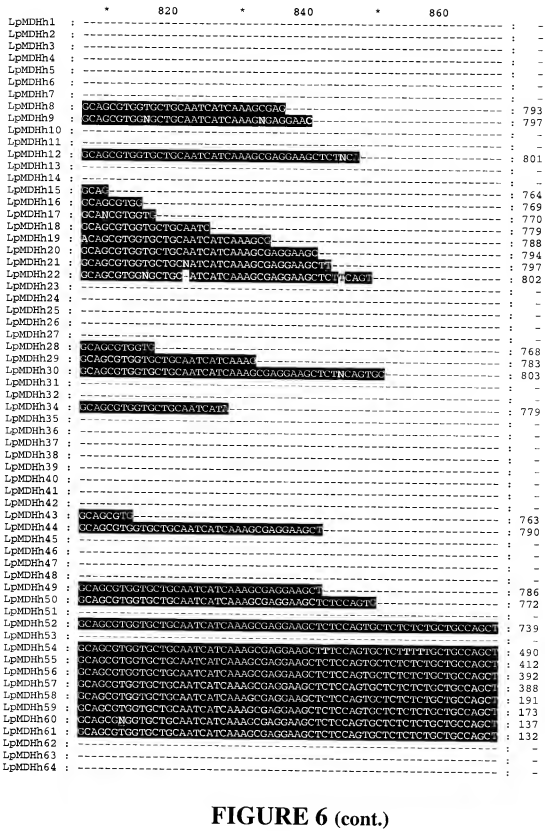


**FIGURE 6 (cont.)**

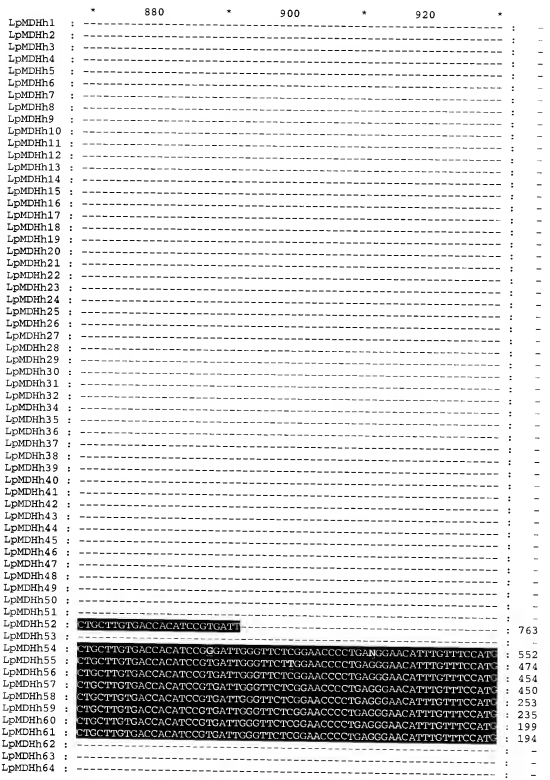


**FIGURE 6 (cont.)**

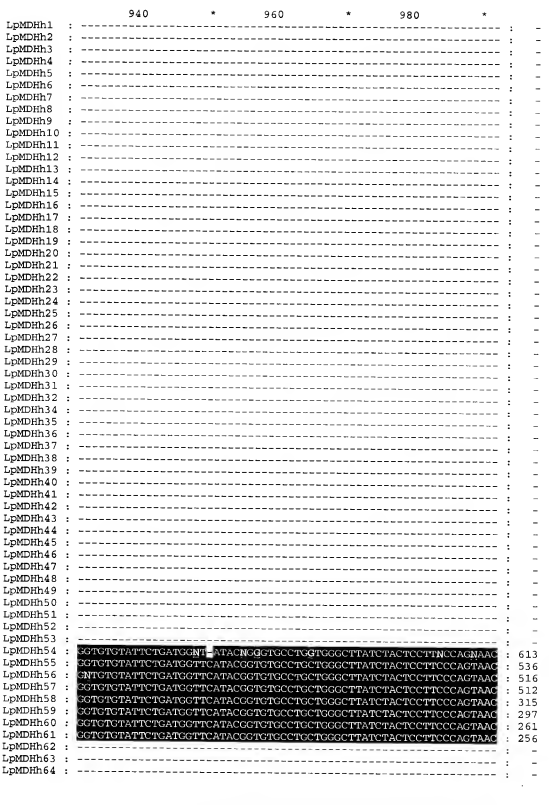


**FIGURE 6 (cont.)**

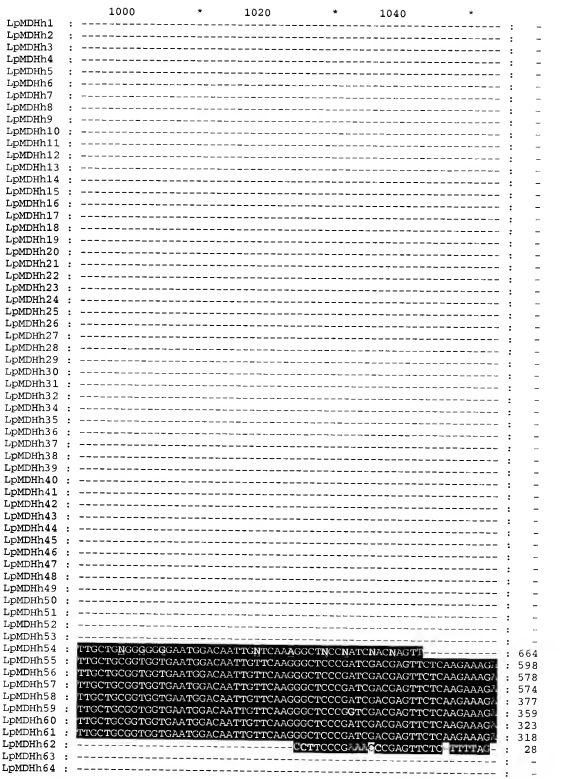


**FIGURE 6 (cont.)**

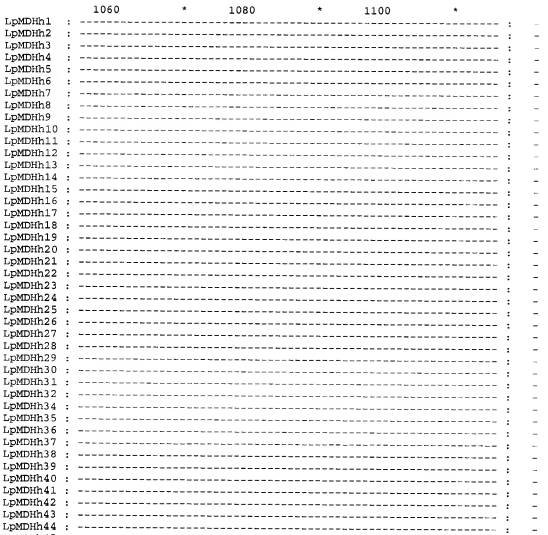


**FIGURE 6 (cont.)**

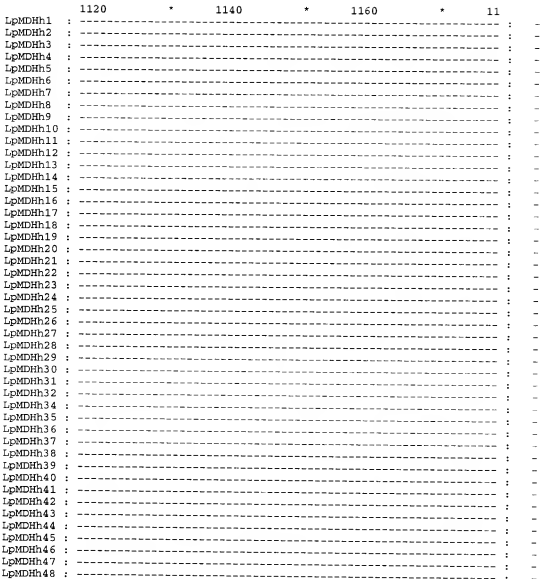


**FIGURE 6 (cont.)**

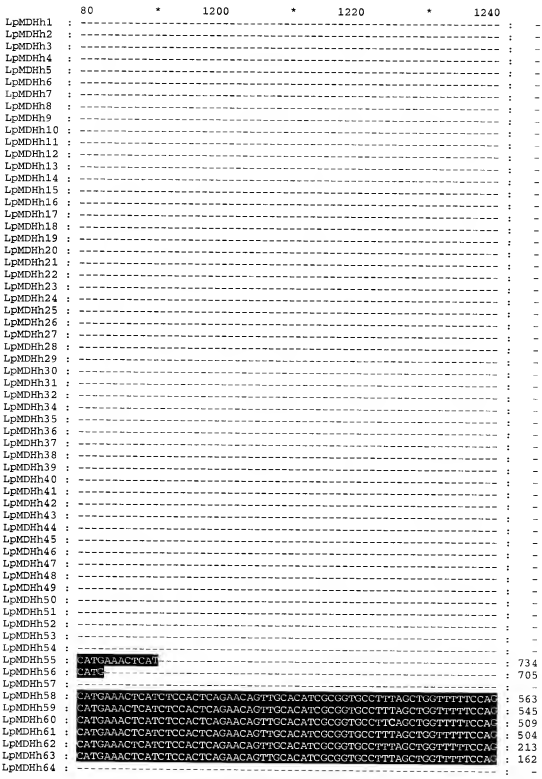


**FIGURE 6 (cont.)**

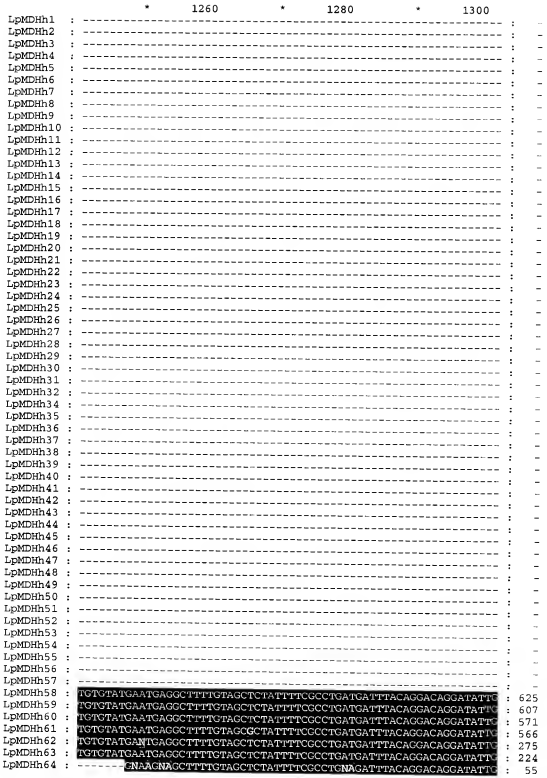


**FIGURE 6 (cont.)**

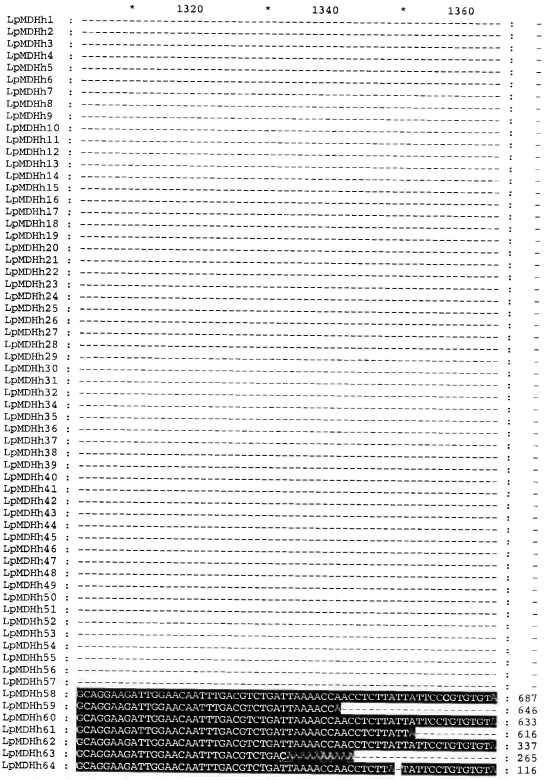


**FIGURE 6 (cont.)**

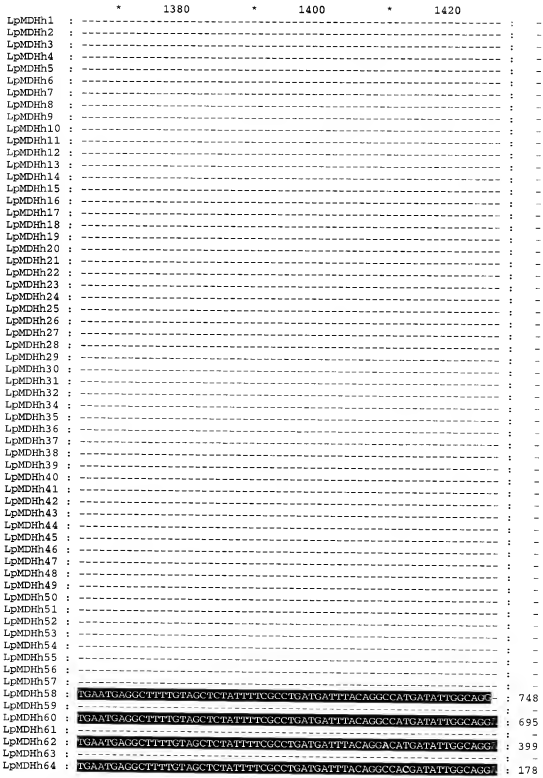


**FIGURE 6 (cont.)**

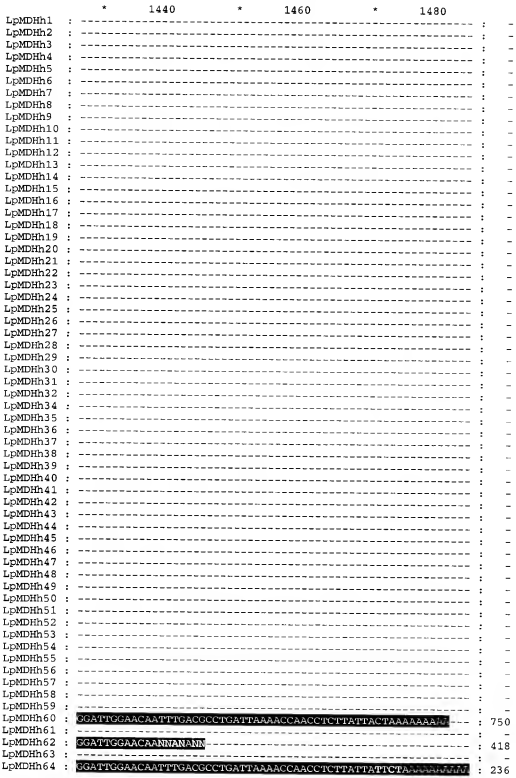


**FIGURE 6 (cont.)**

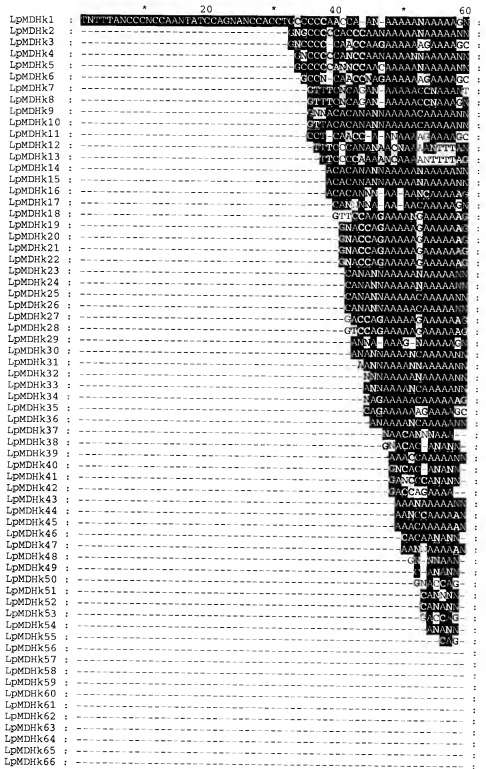
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**FIGURE 7**

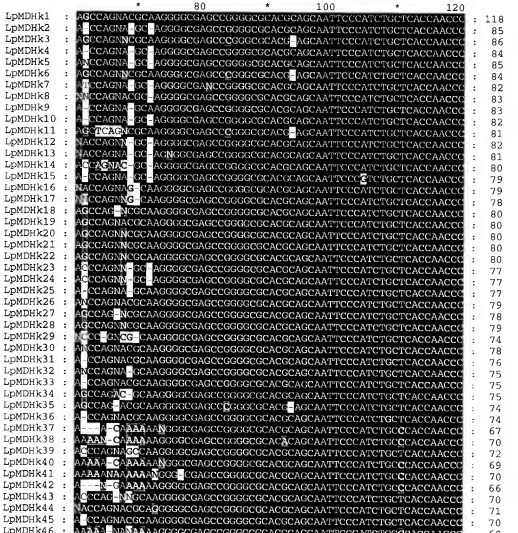


**FIGURE 7 (cont.)**

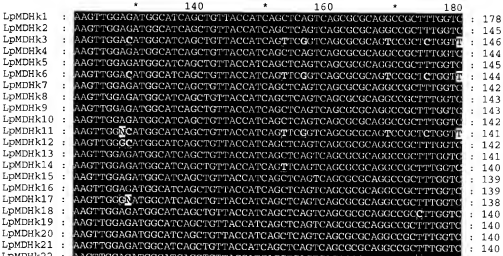



**FIGURE 7 (cont.)**

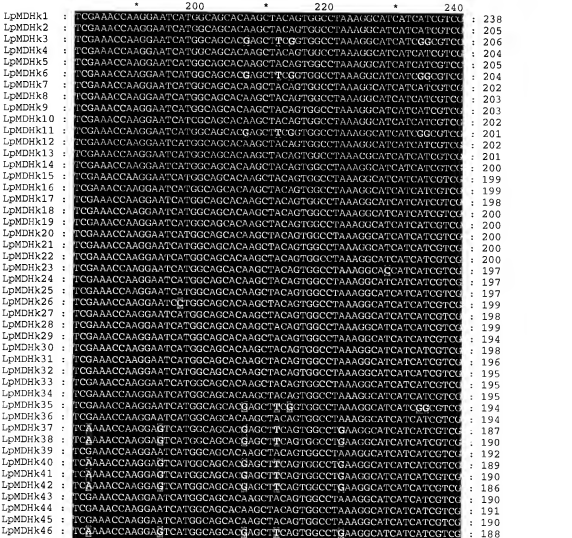



**FIGURE 7 (cont.)**

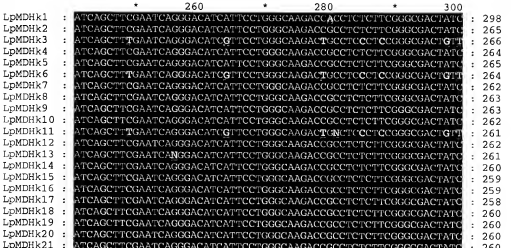



**FIGURE 7 (cont.)**


**FIGURE 7 (cont.)**

FIGURE 7 (cont.)

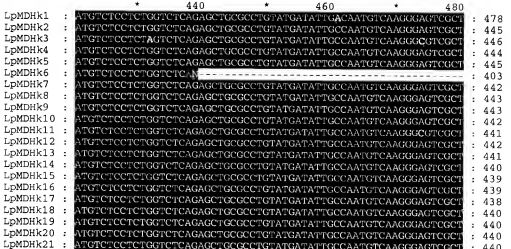



FIGURE 7 (cont.)

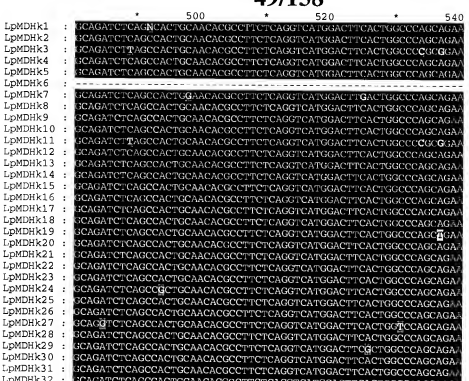


FIGURE 7 (cont.)

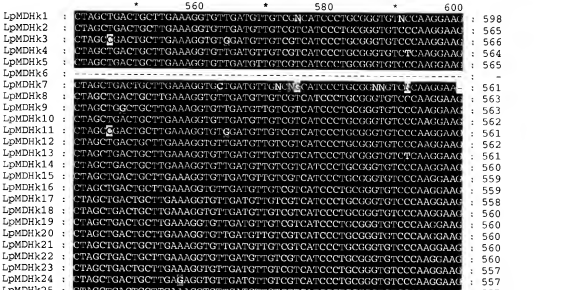


FIGURE 7 (cont.)

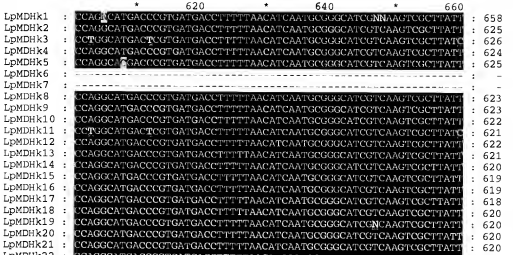



**FIGURE 7 (cont.)**

FIGURE 7 (cont.)


**FIGURE 7 (cont.)**

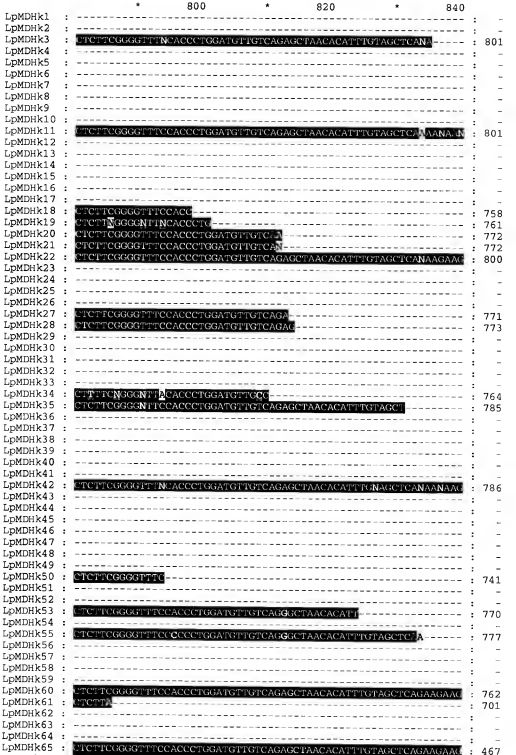



**FIGURE 7 (cont.)**

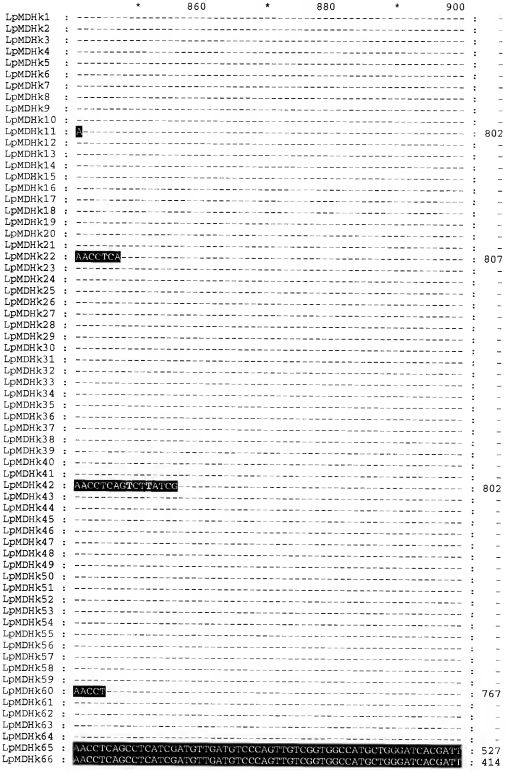



**FIGURE 7 (cont.)**

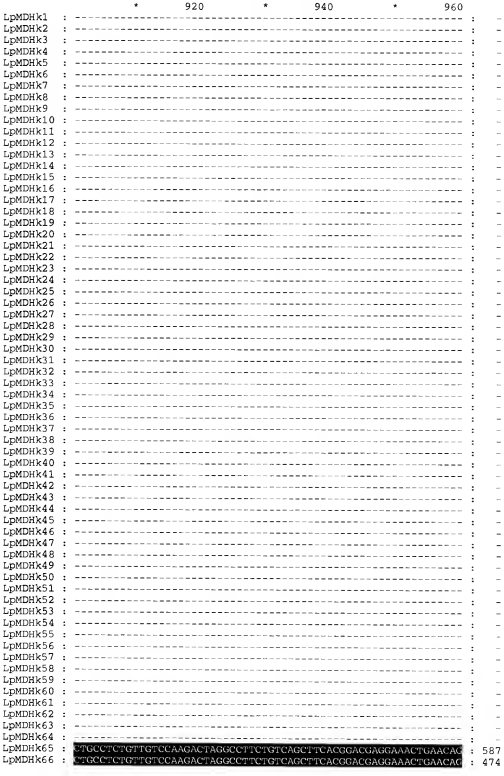



**FIGURE 7 (cont.)**

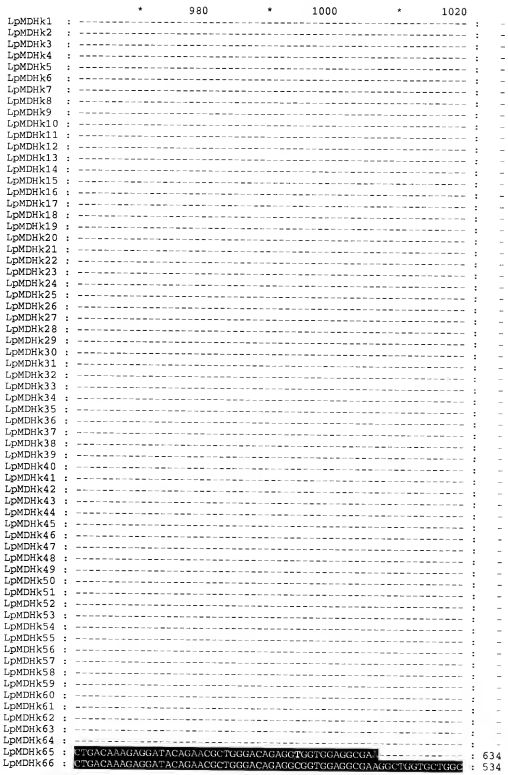



**FIGURE 7 (cont.)**

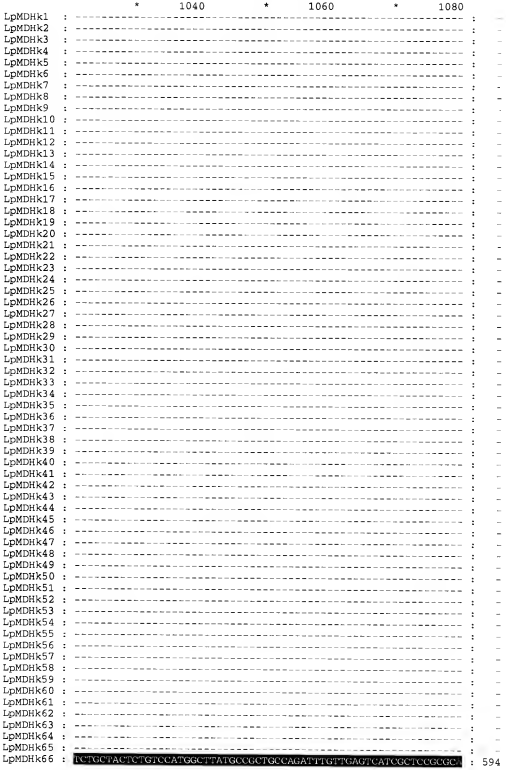



**FIGURE 7 (cont.)**

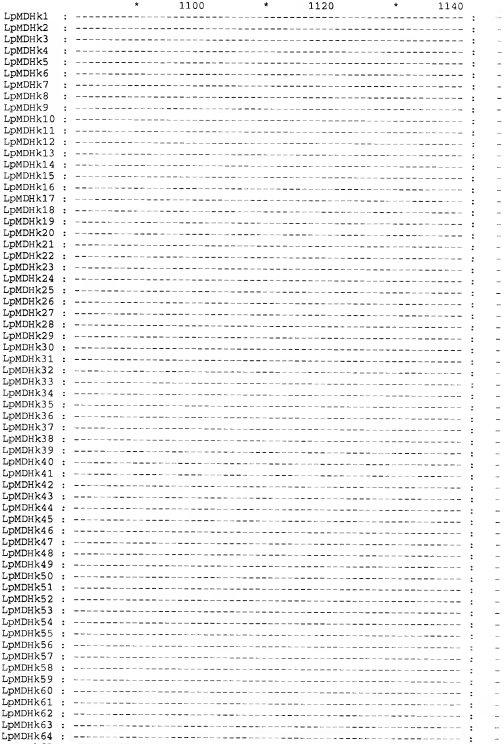



**FIGURE 7 (cont.)**

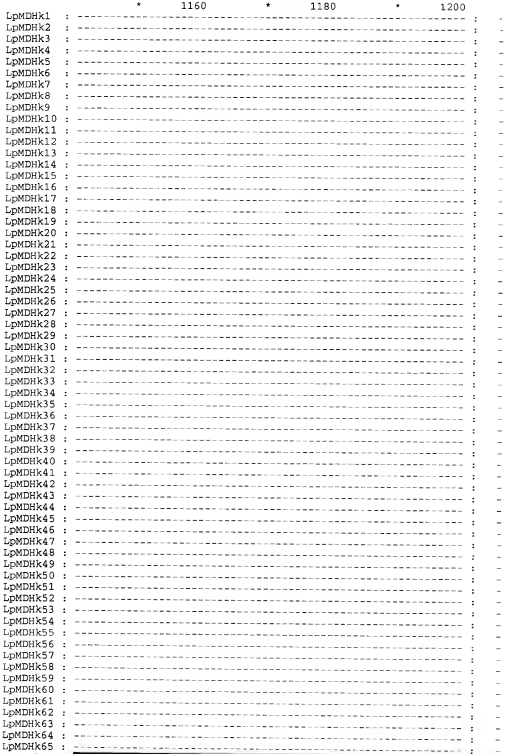



**FIGURE 7 (cont.)**

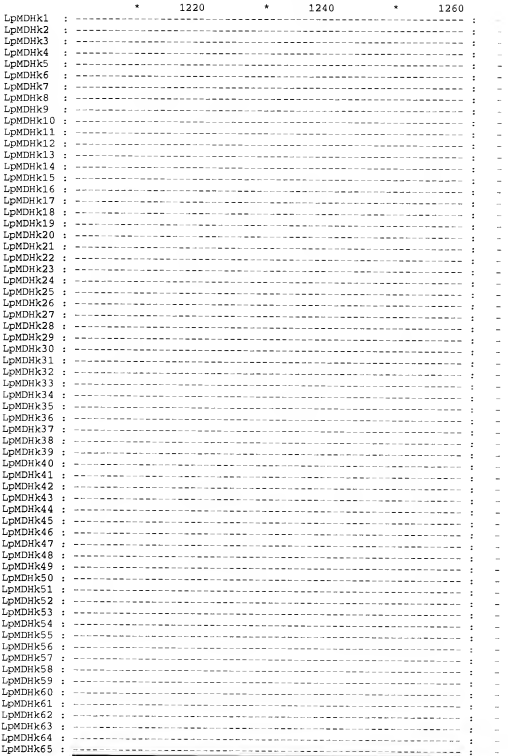



**FIGURE 7 (cont.)**

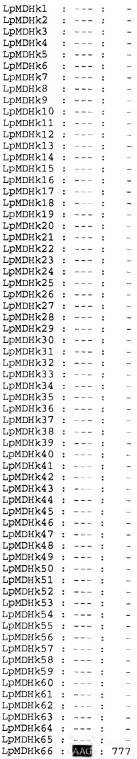
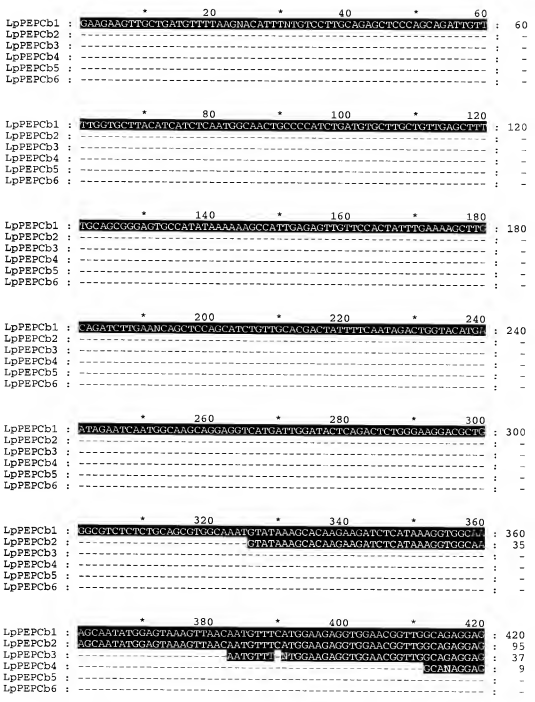



**FIGURE 7 (cont.)**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LpPEPCb2 : ---------- : -
LpPEPCb3 : ---------- : -
LpPEPCb4 : ---------- : -
LpPEPCb5 : ---------- : -
LpPEPCb6 : ---------- : -
LpPEPCb1 : TTGGTGCTTACATCATCTCAATGGCAACTGCCCCATCTGATGTGCTTGCTGTTGAGCTTT : 120
LpPEPCb2 : ---------- : -
LpPEPCb3 : ---------- : -
LpPEPCb4 : ---------- : -
LpPEPCb5 : ---------- : -
LpPEPCb6 : ---------- : -
LpPEPCb1 : TCCAGCGGGAGTGCCATATAAAAAAGCCATTGAGAGTTGTTCCACTATTTGAAAAGCTTT : 180
LpPEPCb2 : ---------- : -
LpPEPCb3 : ---------- : -
LpPEPCb4 : ---------- : -
LpPEPCb5 : ---------- : -
LpPEPCb6 : ---------- : -
LpPEPCb1 : CAGATCTTGAANCAGCTCCAGCATCTGTTGCACGACTATTTTCAATAGACTGGTAGCATGT : 240
LpPEPCb2 : ---------- : -
LpPEPCb3 : ---------- : -
LpPEPCb4 : ---------- : -
LpPEPCb5 : ---------- : -
LpPEPCb6 : ---------- : -
LpPEPCb1 : ATAGAATCAATGGCAAGCAGGAGGTCATGATTGGATACTCAGACTCTGGGAAGGACGCTC : 300
LpPEPCb2 : ---------- : -
LpPEPCb3 : ---------- : -
LpPEPCb4 : ---------- : -
LpPEPCb5 : ---------- : -
LpPEPCb6 : ---------- : -
LpPEPCb1 : GGCGTCTCTCTGCAGCGTGGCAAATGTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA : 360
LpPEPCb2 : ----------GTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA : 35
LpPEPCb3 : ---------- : -
LpPEPCb4 : ---------- : -
LpPEPCb5 : ---------- : -
LpPEPCb6 : ---------- : -
LpPEPCb1 : AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG : 420
LpPEPCb2 : AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG : 95
LpPEPCb3 : ----------AATGTTT TATGGAAGAGGTGGAACGGTTGGCAGAGGAG : 37
LpPEPCb4 : ----------GCANAGGAG : 9
LpPEPCb5 : ---------- : -
LpPEPCb6 : ---------- : -

**FIGURE 8**

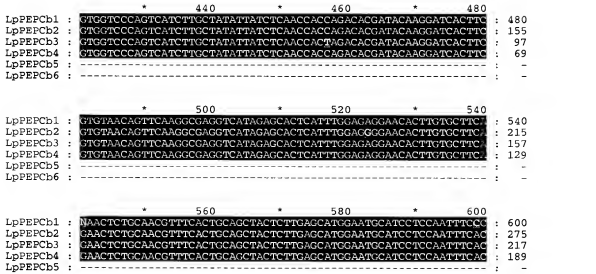
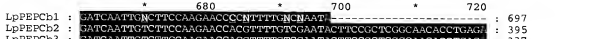



**FIGURE 8 (cont.)**





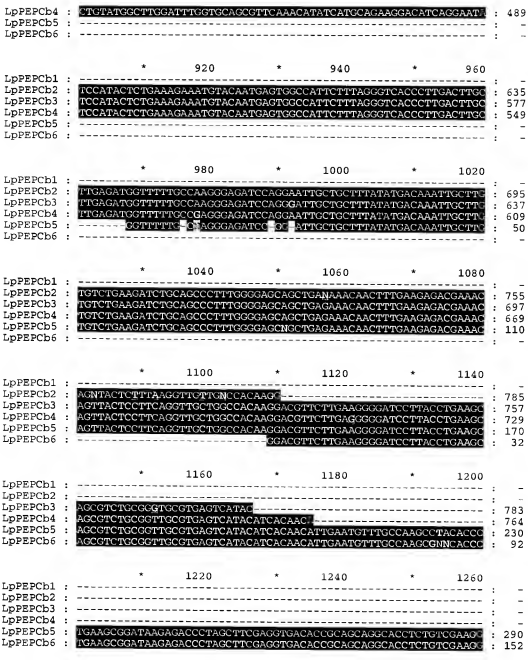



**FIGURE 8 (cont.)**

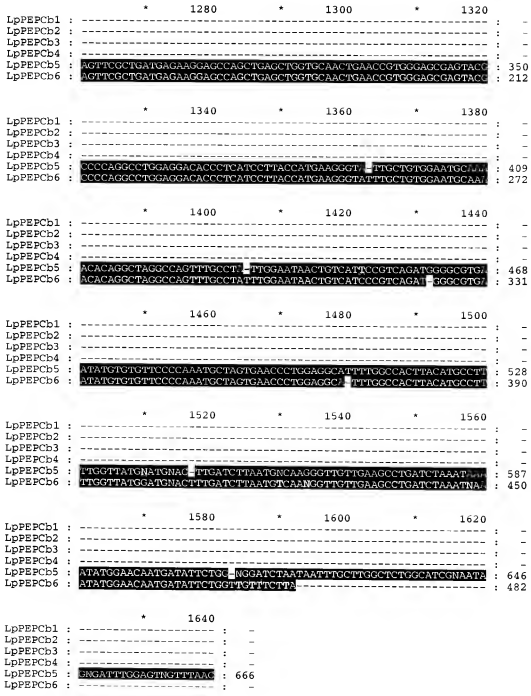
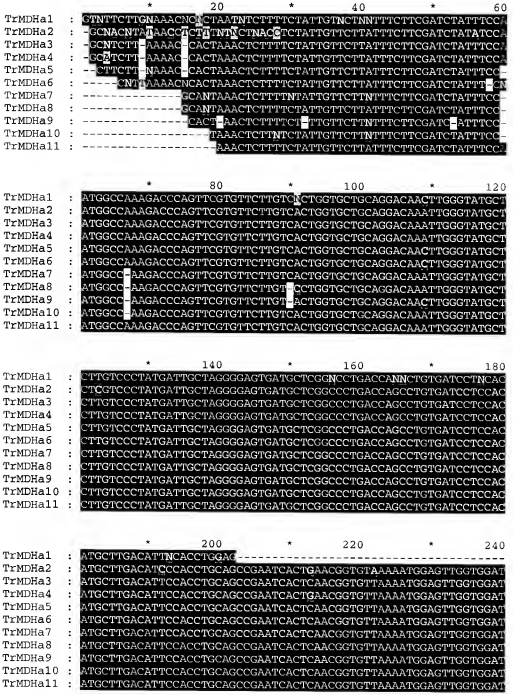



**FIGURE 8 (cont.)**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TrMDHa3 : GCNTCTTTAAAACCACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA : 57
TrMDHa4 : GCATCTTTAAAACCACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA : 57
TrMDHa5 : TTCTTTAAAACCACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCC : 55
TrMDHa6 : CNTTAAAACNCACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCN : 54
TrMDHa7 : GCANTAAACTCTTTTNTATTGTTCTTNTTTCTTCGATCTATTTCC : 45
TrMDHa8 : GCANTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCC : 45
TrMDHa9 : CACTAACTCTTTTCTTTGTTCTTNTTTCTTCGATCTATTTCC : 41
TrMDHa10 : TAAACTCTTNTCTATTGTTCTTNTTTCTTCGATCTATTTCC : 41
TrMDHa11 : AAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCC : 41

TrMDHa1 : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCNCTGGTGCTGCAGGACAACTTGGGTATGCT : 120
TrMDHa2 : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 119
TrMDHa3 : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 117
TrMDHa4 : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 117
TrMDHa5 : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAACTTGGGTATGCT : 115
TrMDHa6 : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAACTTGGGTATGCT : 114
TrMDHa7 : ATGGCCAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 104
TrMDHa8 : ATGCCCAAGACCCAGTTCGTGTTCTTGTCGCTGGTGCTGCAGGACAAATTGGGTATGCT : 103
TrMDHa9 : ATGGCCAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAACTTGGGTATGCT : 99
TrMDHa10 : ATGGCCAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 100
TrMDHa11 : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 101

TrMDHa1 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC : 180
TrMDHa2 : CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 179
TrMDHa3 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 177
TrMDHa4 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 177
TrMDHa5 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 175
TrMDHa6 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 174
TrMDHa7 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 164
TrMDHa8 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 163
TrMDHa9 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 159
TrMDHa10 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 160
TrMDHa11 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 161

TrMDHa1 : ATGCTTGACATTNCACCTGGAG---------- : 202
TrMDHa2 : ATGCTTGACATCCCACCTGCAGCCGAATCACTGAACGGTGTTAAAAATGGAGTTGGTGGAT : 239
TrMDHa3 : ATGCTTGACATCCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 237
TrMDHa4 : ATGCTTGACATTCCACCTGCAGCCGAATCACTGAACGGTGTTAAAATGGAGTTGGTGGAT : 237
TrMDHa5 : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 235
TrMDHa6 : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 234
TrMDHa7 : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 224
TrMDHa8 : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 223
TrMDHa9 : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 219
TrMDHa10 : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 220
TrMDHa11 : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 221

FIGURE 9

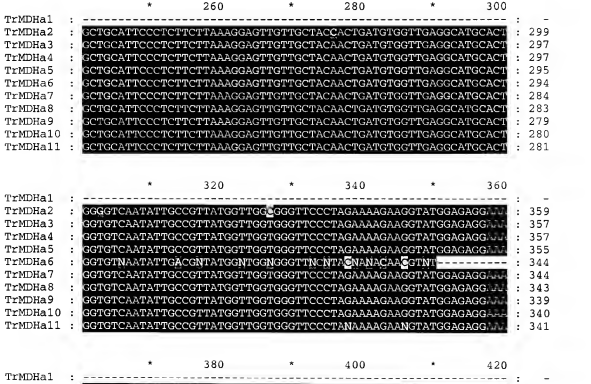


**FIGURE 9 (cont.)**

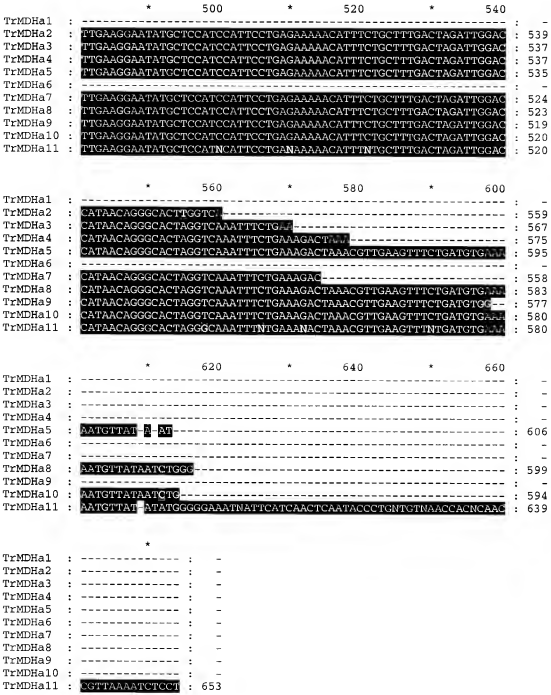


**FIGURE 9 (cont.)**

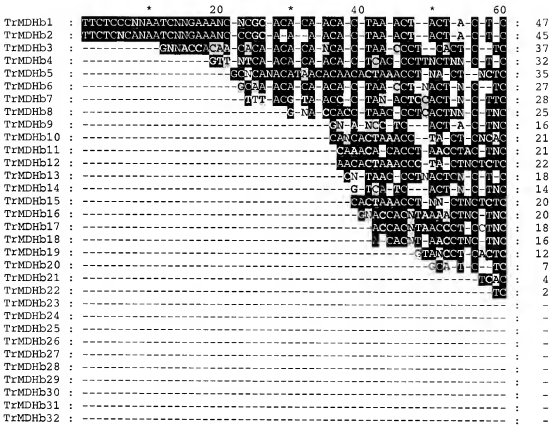

FIGURE 10

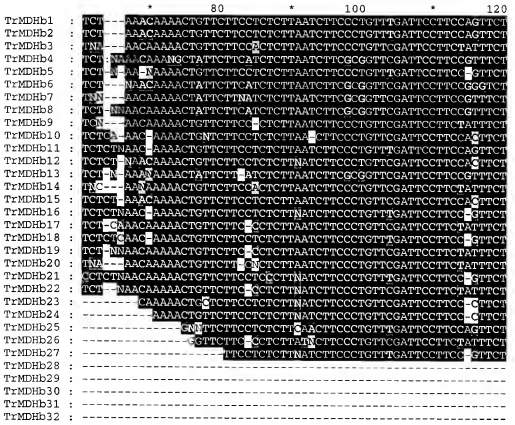


**FIGURE 10 (cont.)**

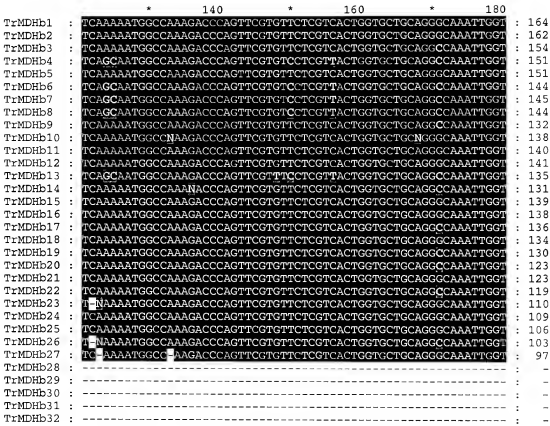


**FIGURE 10 (cont.)**

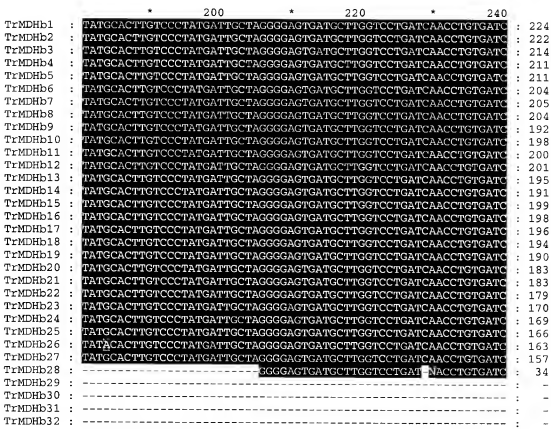


**FIGURE 10 (cont.)**

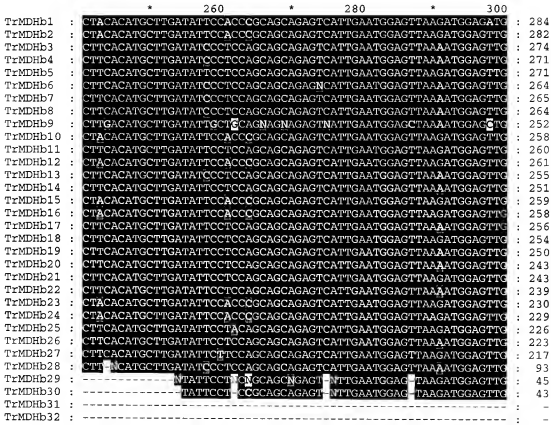


**FIGURE 10 (cont.)**

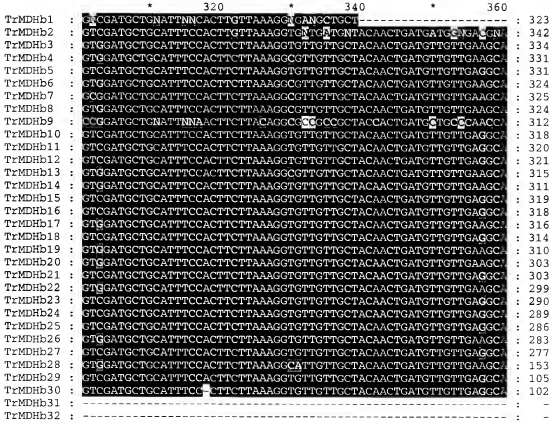


**FIGURE 10 (cont.)**

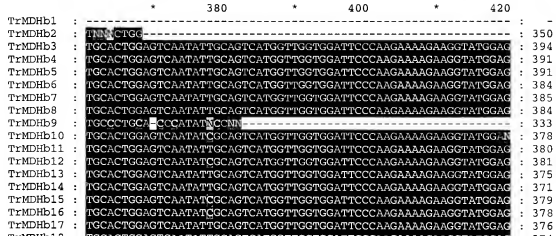


**FIGURE 10 (cont.)**

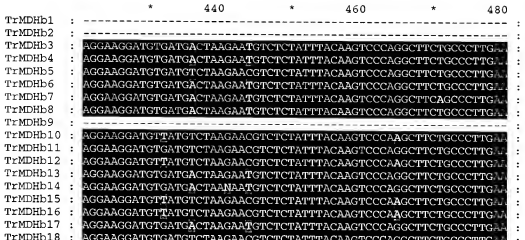


**FIGURE 10 (cont.)**

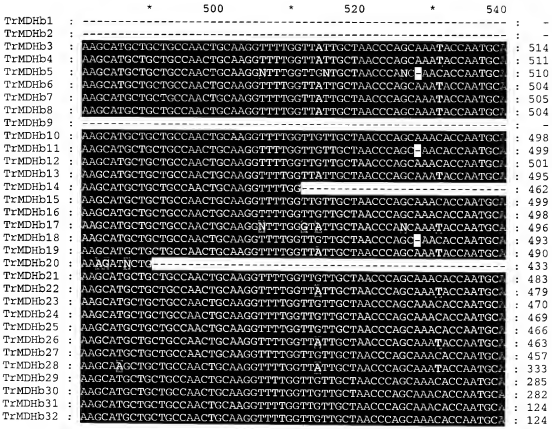


**FIGURE 10 (cont.)**

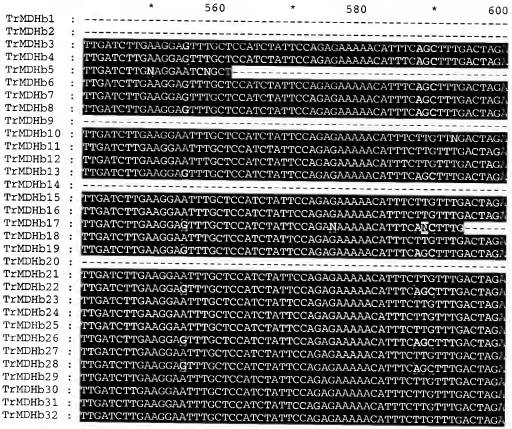


**FIGURE 10 (cont.)**

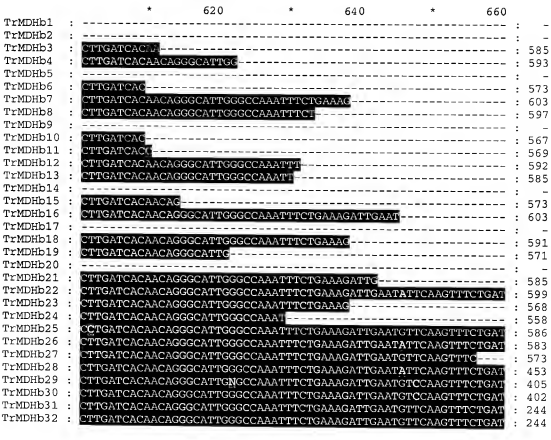


**FIGURE 10 (cont.)**

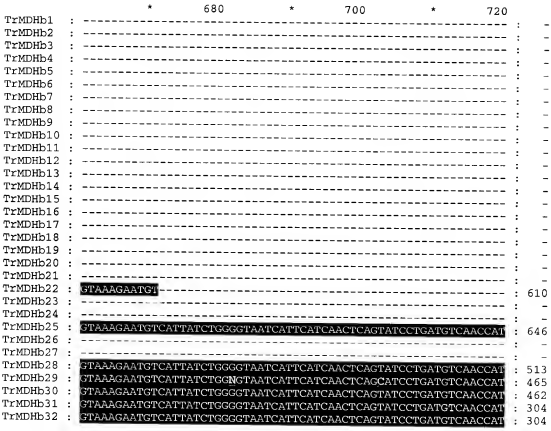


**FIGURE 10 (cont.)**

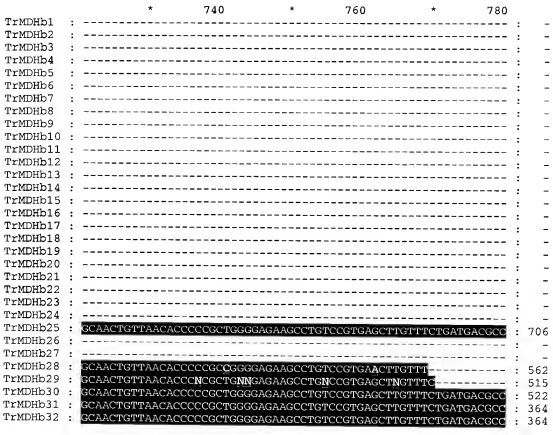


**FIGURE 10 (cont.)**

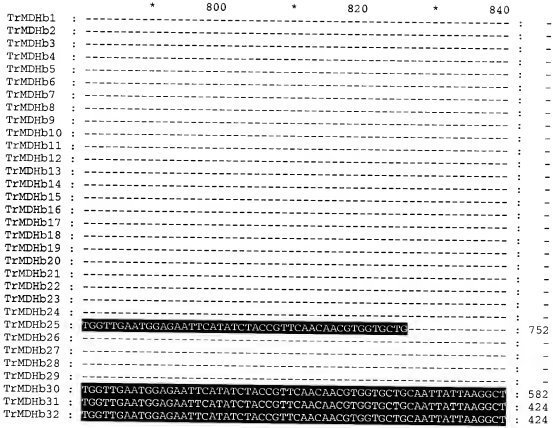


**FIGURE 10 (cont.)**

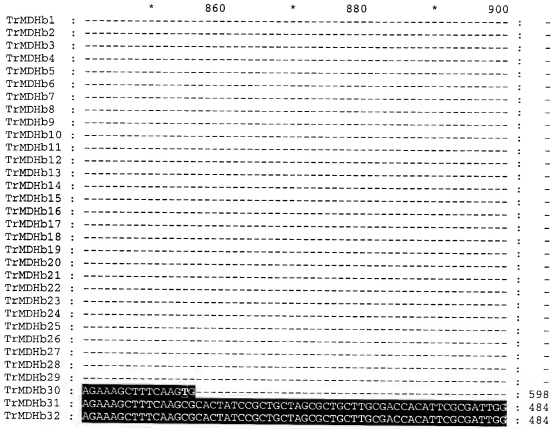


**FIGURE 10 (cont.)**

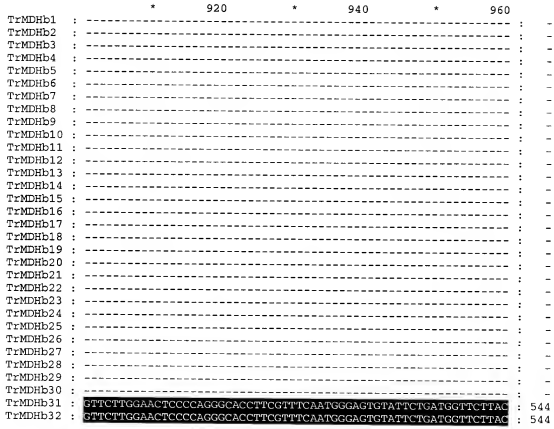


**FIGURE 10 (cont.)**

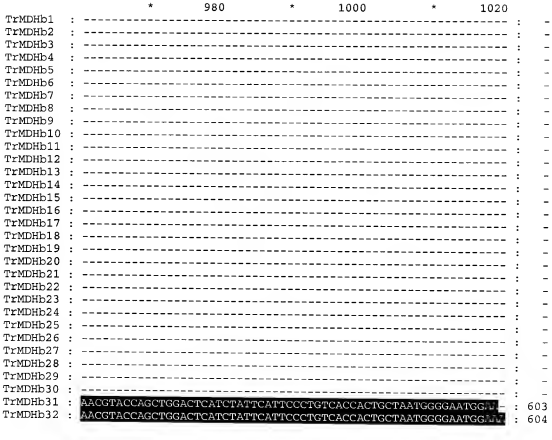


**FIGURE 10 (cont.)**

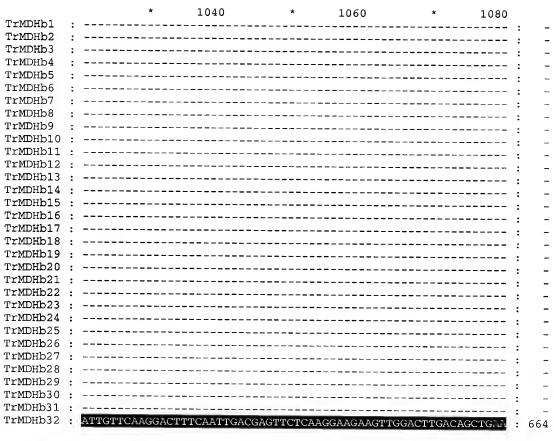


**FIGURE 10 (cont.)**

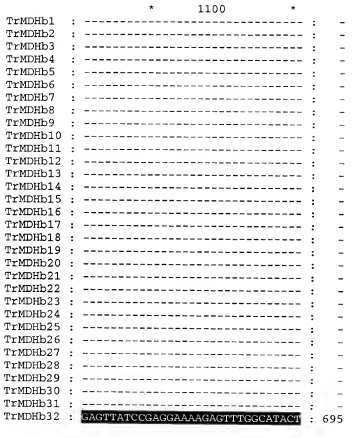


**FIGURE 10 (cont.)**

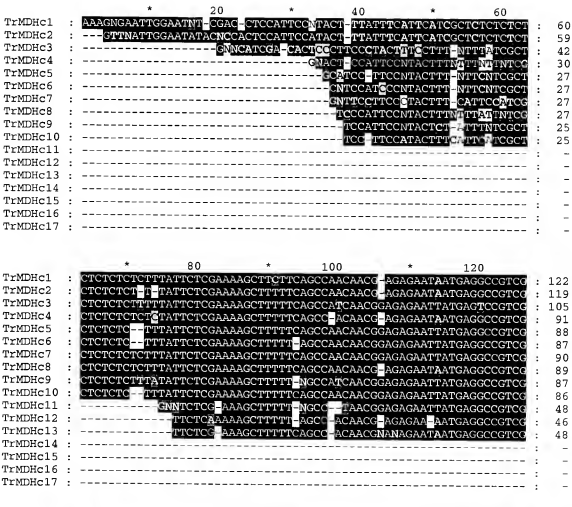


**FIGURE 11**

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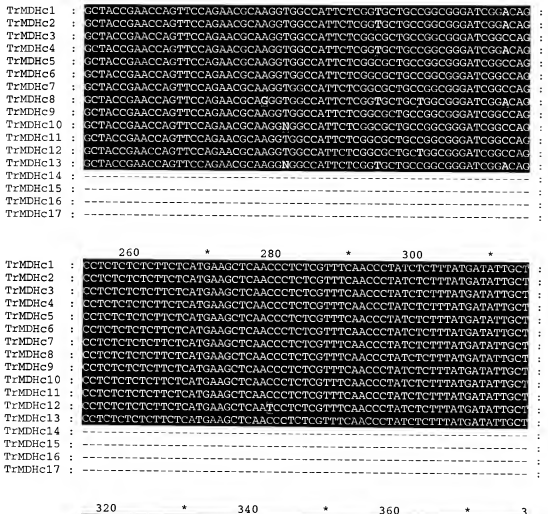


**FIGURE 11 (cont.)**

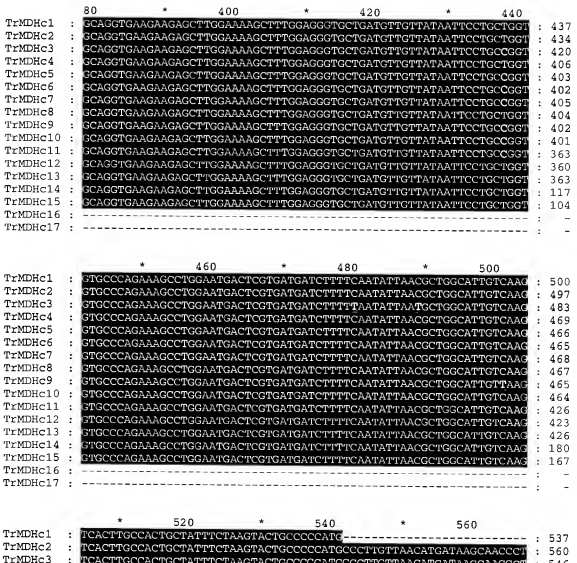


**FIGURE 11 (cont.)**

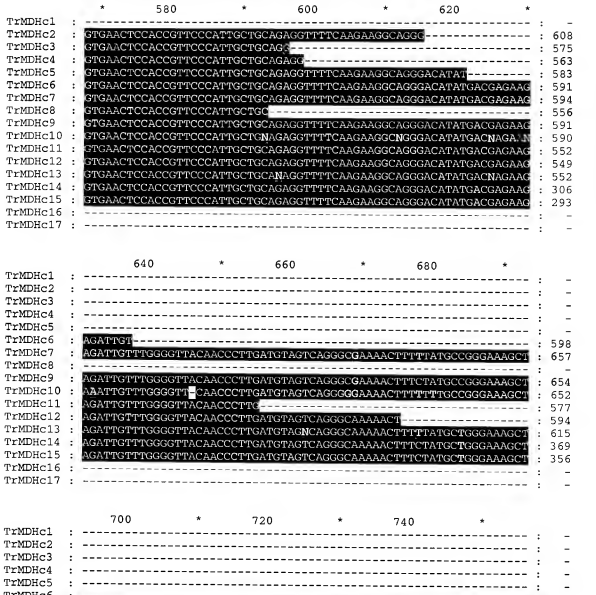


**FIGURE 11 (cont.)**

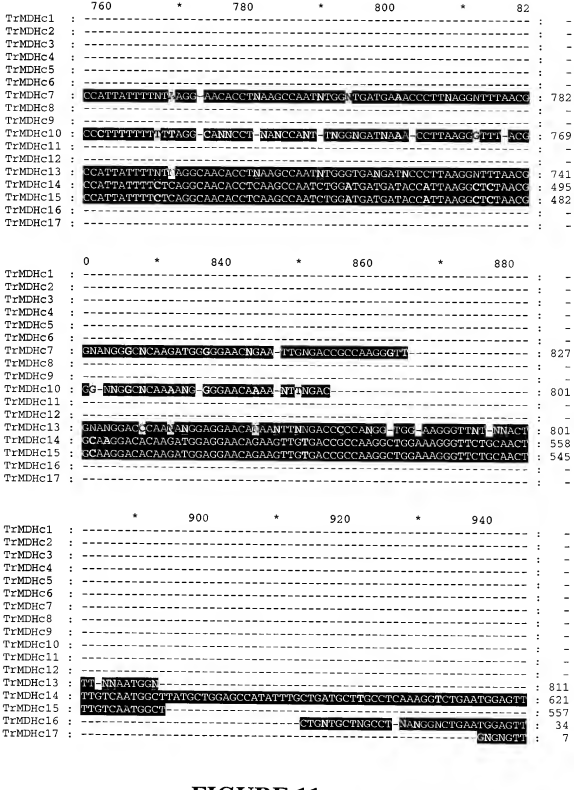


**FIGURE 11 (cont.)**

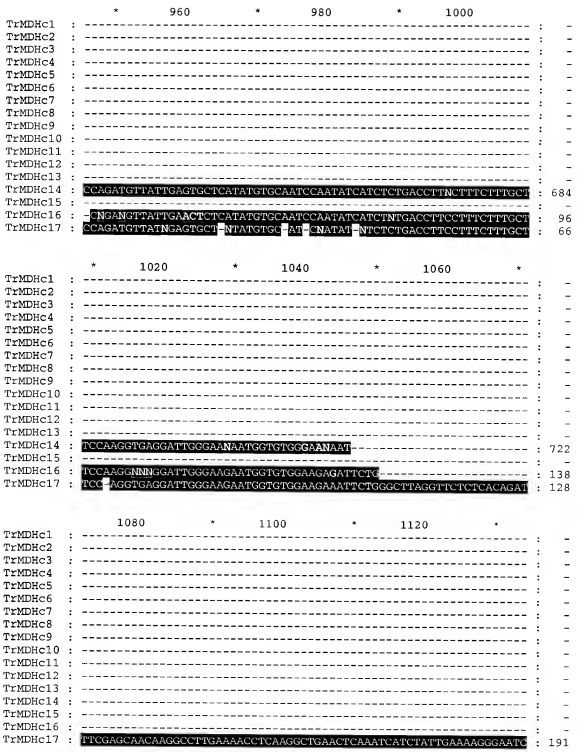


**FIGURE 11 (cont.)**

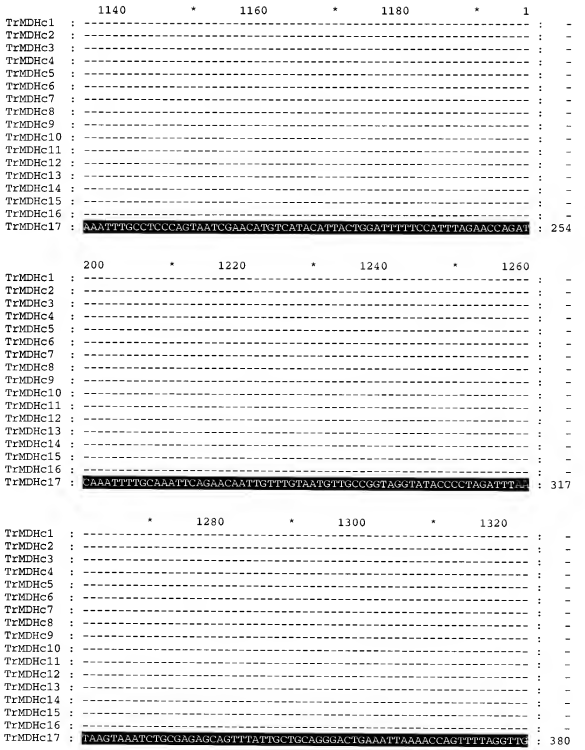


**FIGURE 11 (cont.)**

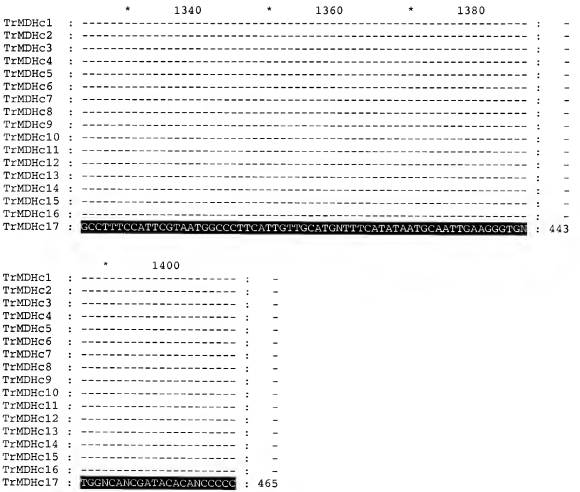


**FIGURE 11 (cont.)**

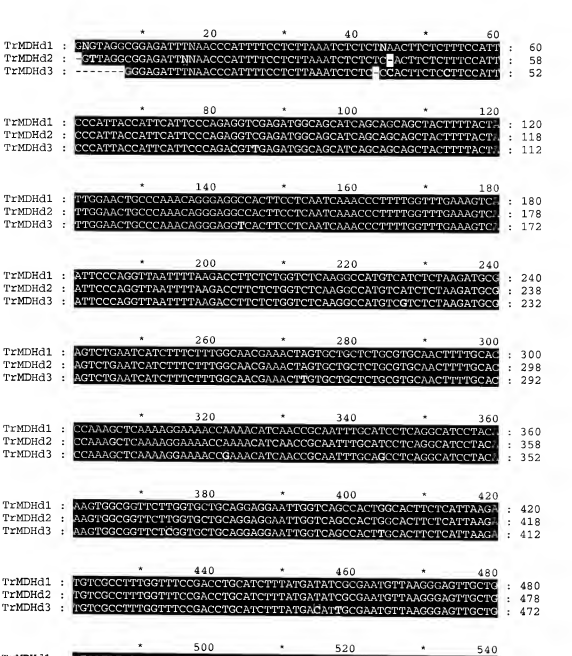
TrMDHd1 : GNGTAGGCGGAGATTTNAACCCATTTTCCTCTTAAATCTCTCTNAACTTCTCTTTCCATT : 60
TrMDHd2 : -GTTAGGCGGAGATTNNAACCCATTTTCCTCTTAAATCTCTCTG-ACTTCTCTTTCCATT : 58
TrMDHd3 : -------GGGAGATTTNAACCCATTTTCCTCTTAAATCTCTG-CCACTTCTCCTTCCATT : 52
TrMDHd1 : CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTT : 120
TrMDHd2 : CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTT : 118
TrMDHd3 : CCCATTACCATTCATTCCCAGACGTTGAGATGGCAGCATCAGCAGCAGCTACTTTTACTT : 112
TrMDHd1 : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCT : 180
TrMDHd2 : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCT : 178
TrMDHd3 : TTGGAACTGCCCAAACAGGGAGGTCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCT : 172
TrMDHd1 : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 240
TrMDHd2 : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 238
TrMDHd3 : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCGTCTCTAAGATGCG : 232
TrMDHd1 : AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC : 300
TrMDHd2 : AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC : 298
TrMDHd3 : AGTCTGAATCATCTTTCTTTGGCAACGAAACTTGTGCTGCTCTGCGTGCAACTTTTGCAC : 292
TrMDHd1 : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTTGCATCCTCAGGCATCCTACT : 360
TrMDHd2 : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTTGCATCCTCAGGCATCCTACT : 358
TrMDHd3 : CCAAAGCTCAAAAGGAAAACCGAAACATCAACCGCAATTTGCAGCCTCAGGCATCCTACT : 352
TrMDHd1 : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTCTGGCACTTCTCATTAAGA : 420
TrMDHd2 : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTTCTCATTAAGA : 418
TrMDHd3 : AAGTGGCGGTTCTCGGTGCTGCAGGAGGAATTGGTCAGCCACTTGCACTTCTCATTAAGA : 412
TrMDHd1 : TGTCGCCTTTGGTTTCGGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 480
TrMDHd2 : TGTCGCCTTTGGTTTCGGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 478
TrMDHd3 : TGTCGCCTTTGGTTTCGGACCTGCATCTTTATGACATTGCGAATGTTAAGGGAGTTGCTG : 472
TrMDHd1 : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGT : 540
TrMDHd2 : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGT : 538
TrMDHd3 : CTGATATCAGCCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGC : 532
TrMDHd1 : TGGCAAATTGTTTG---------- : 554
TrMDHd2 : TGGCAAATTGTTTGAAAGGTGTGGATGTAGTTGTTATACCTGCTGGTGTTCCCAG--- : 593
TrMDHd3 : TAGCAAATTGTTTGAAAGGTGTGGATGTTGTTGTTATACCTGCTGGTGTTCCTAGAAA : 590

**FIGURE 12**

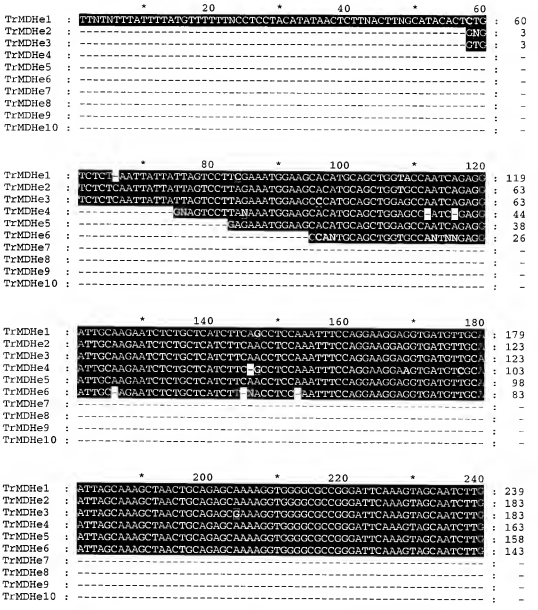
TrMDHe1 : TTWTNTTTATTTTATGTTTTTTNCCTCCTACATATAACTCTTNACTTNGCATACACTCTG : 60
TrMDHe2 : ----------GNG : 3
TrMDHe3 : ----------GTG : 3
TrMDHe4 : ---------- : -
TrMDHe5 : ---------- : -
TrMDHe6 : ---------- : -
TrMDHe7 : ---------- : -
TrMDHe8 : ---------- : -
TrMDHe9 : ---------- : -
TrMDHe10 : ---------- : -
TrMDHe1 : TCTCT-AATTATTATTAGTCCTTCGAAATGGAAGCACATGCAGCTGGTACCAATCAGAGG : 119
TrMDHe2 : TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGTGCCAATCAGAGG : 63
TrMDHe3 : TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCCCATGCAGCTGGAGCCAATCAGAGG : 63
TrMDHe4 : ----------GNAGTCCTTANAAATGGAAGCACATGCAGCTGGAGCC-ATC-GAGG : 44
TrMDHe5 : ----------GAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG : 38
TrMDHe6 : ----------CCANTGCAGCTGGTGCCANTNNGAGG : 26
TrMDHe7 : ---------- : -
TrMDHe8 : ---------- : -
TrMDHe9 : ---------- : -
TrMDHe10 : ---------- : -
TrMDHe1 : ATTGCAAGAATCTCTGCTCATCTTCAGCCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 179
TrMDHe2 : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 123
TrMDHe3 : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGCAAGGAGGTGATGTTGCA : 123
TrMDHe4 : ATTGCAAGAATCTCTGCTCATCTTC-GCCTCCAAATTTCCAGGAAGGAAGTGATGTCGC : 103
TrMDHe5 : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 98
TrMDHe6 : ATTGG-AGAATCTCTGCTCATCTT-NACCTCC-AATTTCCAGGAAGGAGGTGATGTTGCA : 83
TrMDHe7 : ---------- : -
TrMDHe8 : ---------- : -
TrMDHe9 : ---------- : -
TrMDHe10 : ---------- : -
TrMDHe1 : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 239
TrMDHe2 : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 183
TrMDHe3 : ATTAGCAAAGCTAACTGCAGAGCGAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 183
TrMDHe4 : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAGTAGCAATCTTG : 163
TrMDHe5 : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 158
TrMDHe6 : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 143
TrMDHe7 : ---------- : -
TrMDHe8 : ---------- : -
TrMDHe9 : ---------- : -
TrMDHe10 : ---------- : -

**FIGURE 13**

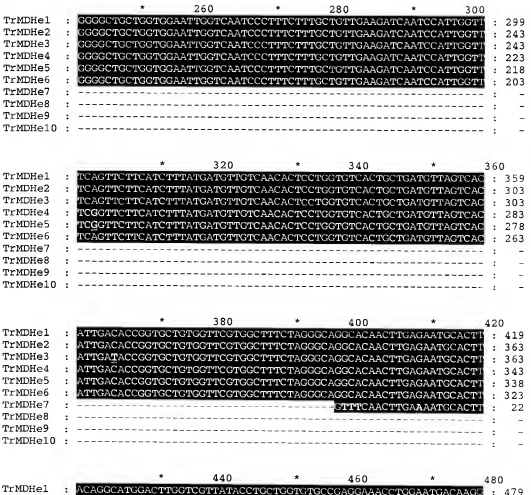


**FIGURE 13 (cont.)**

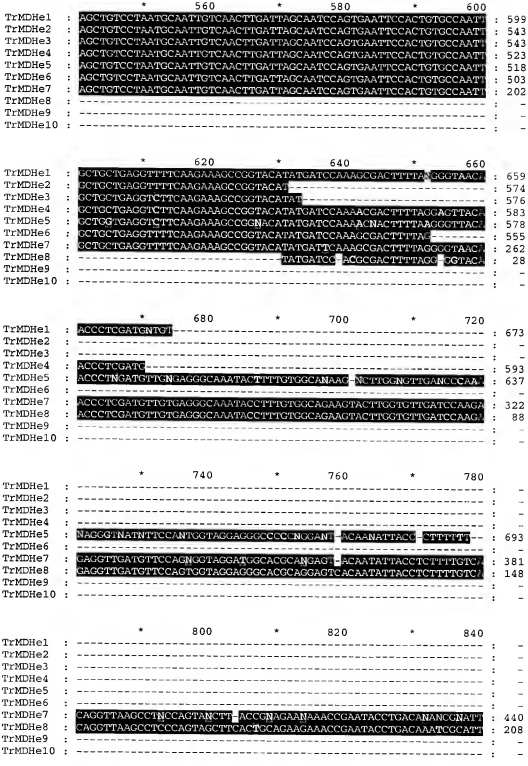


**FIGURE 13 (cont.)**

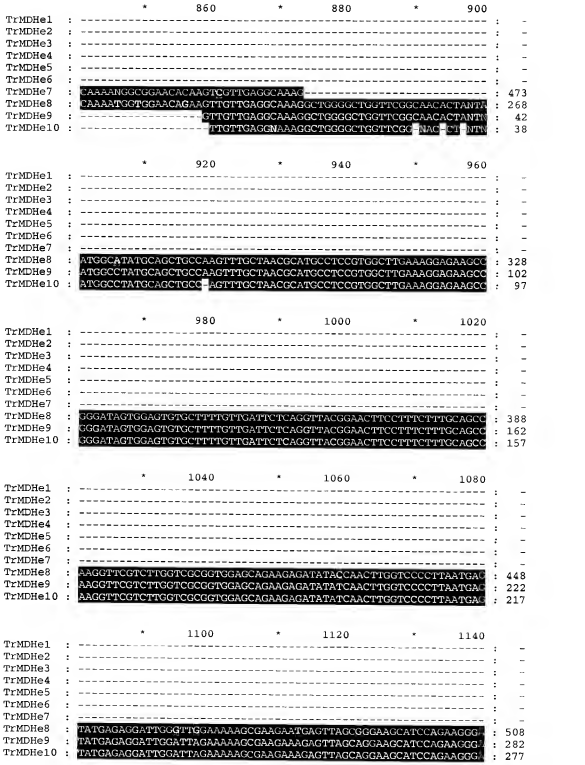


**FIGURE 13 (cont.)**

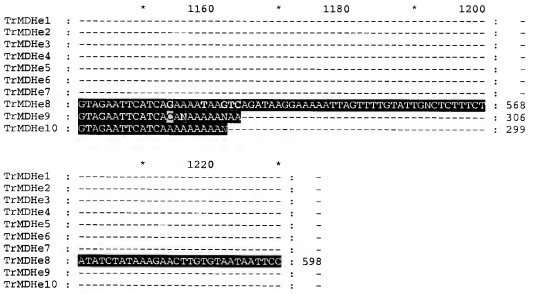


**FIGURE 13 (cont.)**

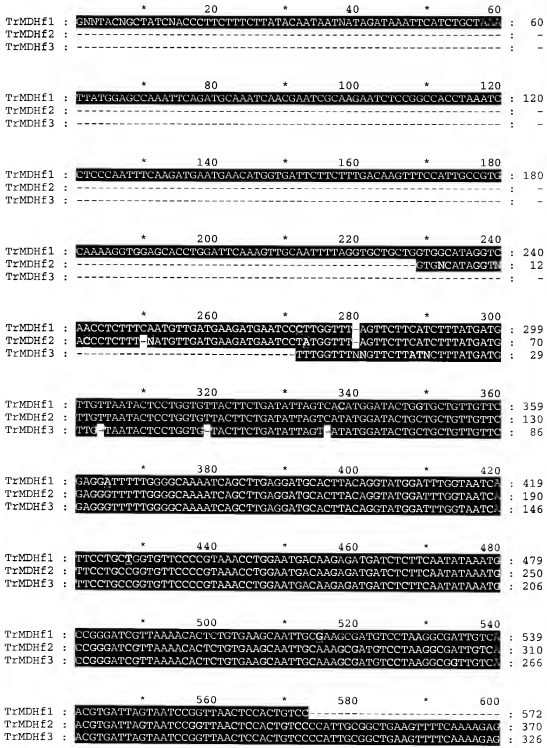


FIGURE 14

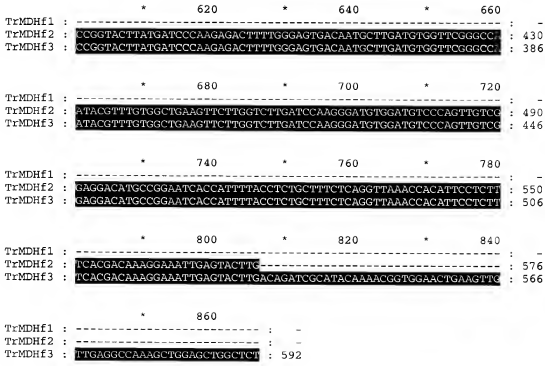


**FIGURE 14 (cont.)**

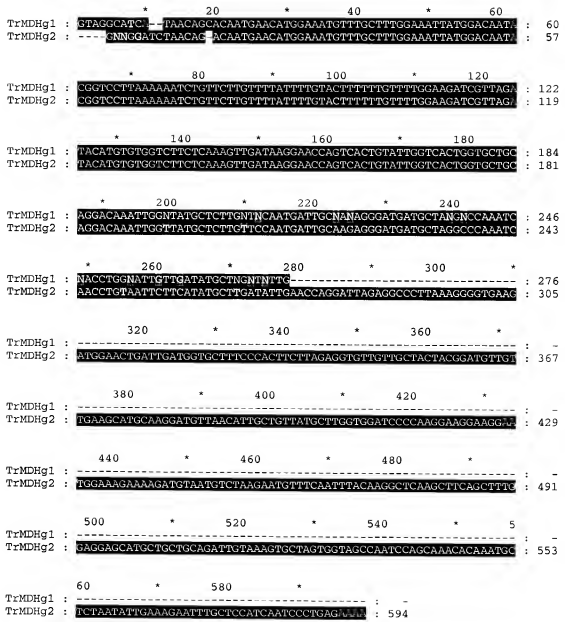
TrMDHg1 : GTAGGCATC--TAACAGCACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAATA : 60
TrMDHg2 : ----GNNGGATCTAACAG-ACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAATA : 57
TrMDHg1 : CGGTCCTTAAAAAATCNGTTCTTGTTTTATTTTGTACTTTTTTGTTTTGGAAGATCGTTAGA : 122
TrMDHg2 : CGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTGTTTTGGAAGATCGTTAGA : 119
TrMDHg1 : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 184
TrMDHg2 : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 181
TrMDHg1 : AGGACAAATTGGNTATGCTCTTGNTNCAATGATTGCNANAGGGATGATGCTANGNCCAAATC : 246
TrMDHg2 : AGGACAAATTGGTTATGCTCTTGTTCCAATGATTGCAAGAGGGATGATGCTAGGCCCAAATC : 243
TrMDHg1 : NACCTGGNATTGTTGATATGCTNGNTNTTC---------- : 276
TrMDHg2 : AACCTGTAATTCTTCATATGCTTGATATTGAACCAGGATTAGAGGCCCTTAAAGGGGTGAAG : 305
TrMDHg1 : ---------- : -
TrMDHg2 : ATGGAACTGATTGATGGTGCTTTCCCACTTCTTAGAGGTGTTGTTGCTACTACGGATGTTGT : 367
TrMDHg1 : ---------- : -
TrMDHg2 : TGAAGCATGCAAGGATGTTAACATTGCTGTTATGCTTGGTGGATCCCCAAGGAAGGAAGGAG : 429
TrMDHg1 : ---------- : -
TrMDHg2 : TGGAAAGAAAAGATGTAATGTCTAAGAATGTTTCAATTTACAAGGCTCAAGCTTCAGCTTTG : 491
TrMDHg1 : ---------- : -
TrMDHg2 : GAGGAGCATGCTGCTGCAGATTGTAAAGTGCTAGTGGTAGCCAATCCAGCAAACACAAATGC : 553
TrMDHg1 : ---------- : -
TrMDHg2 : TCTAATATTGAAAGAATTTGCTCCATCAATCCCTGAGAAAA : 594

**FIGURE 15**

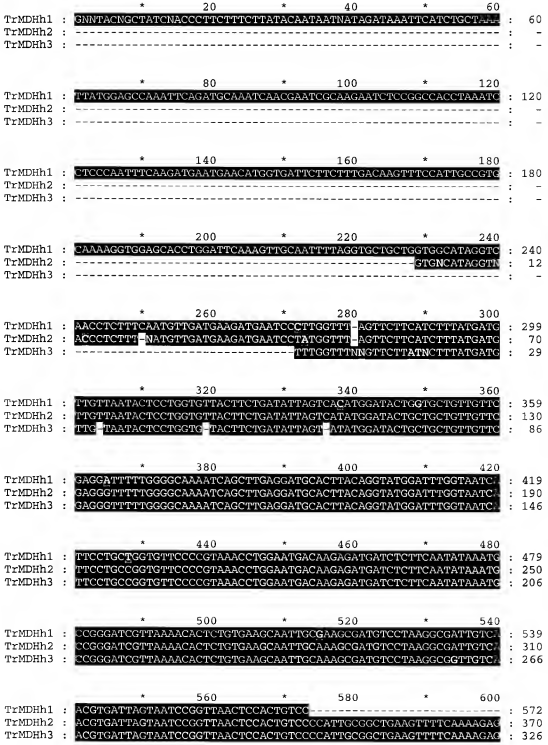


**FIGURE 16**
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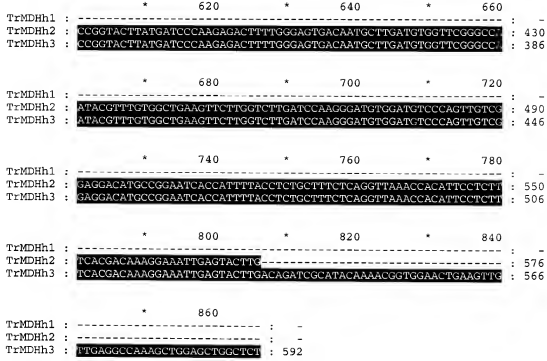


**FIGURE 16 (cont.)**

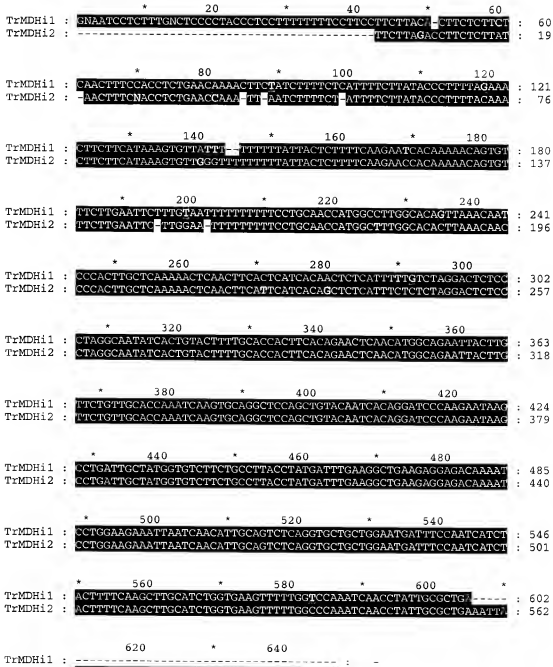


**FIGURE 17**
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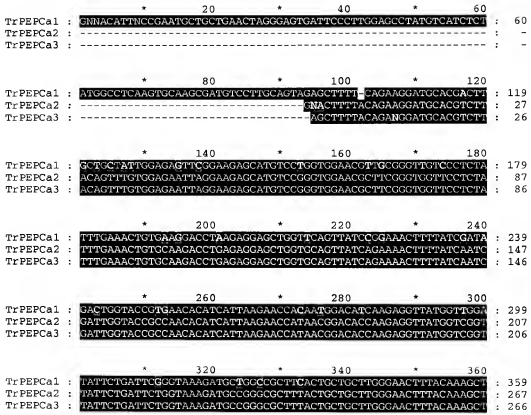
TrPEPCa1 : GNNACATTNCCGAATGCTGCTGAACTAGGGAGTGATTCCCTTGGAGCCTATGTCATCTCT : 60
TrPEPCa2 : ------------------------------------------------------------ : -
TrPEPCa3 : ------------------------------------------------------------ : -
TrPEPCa1 : ATGGCCTCAAGTGCAAGCGATGTCCTTGCAGTAGAGCTTTT-CAGAAGGATGCACGACTT : 119
TrPEPCa2 : ----------------------------GNACTTTTACAGAAGGATGCACGTCTT : 27
TrPEPCa3 : ----------------------------AGCTTTTACAGANGGATGCACGTCTT : 26
TrPEPCa1 : GCTCCATTGGAGAGTTCCGAAGAGCATGTCCTGGTGGAACGTTCGGGTGTTCCCTCTA : 179
TrPEPCa2 : ACAGTTTGTCGGAGAATTAGGAAGAGCATGTCCGGGTGGAACGCTTCGGGTGGTTCCTCTA : 87
TrPEPCa3 : ACAGTTTGTGGAGAATTAGGAAGAGCATGTCCGGGTGGAACGCTTCGGGTGGTTCCTCTA : 86
TrPEPCa1 : TTTGAAACTGTGAAGAGCCTAGAGAGGAGCTGGTTCAGTTATCCGAAACTTTTATCGATA : 239
TrPEPCa2 : TTTGAAACTGTGCAAGACCTGAGAGGAGCTGGTCCAGTTATCAGAAAACTTTTATCAATC : 147
TrPEPCa3 : TTTCAAACTGTGCAAGACCTGAGAGGAGCTGGTCCAGTTATCAGAAAACTTTTATCAATC : 146
TrPEPCa1 : GACTGGTACCGTGAACACATCATTAAGAACCACAAGGGACATCAAGAGGTTATGGTTGGT : 299
TrPEPCa2 : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 207
TrPEPCa3 : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 206
TrPEPCa1 : TATTCTGATTCGGCTAAAGATGCTGCCGCTTCACTGCTGCTTGGGAACTTTACAAAGCT : 359
TrPEPCa2 : TATTCTGATTCTGGTAAAGATGCCGGGGCGCTTTACTGCTGCTTGGGAACTTTACAAAGCT : 267
TrPEPCa3 : TATTCTGATTCTGGTAAAGATGCCGGGGCGCTTTACTGCTGCTTGGGAACTTTACAAAGCT : 266
TrPEPCa1 : CAGGAGGATGTTCTAGCTGCTTGCAATGATTATGGTATTAAGTTACACTGTTTCATGGC : 419
TrPEPCa2 : CAAGAGGATGTAGTGGCTGCTTGCAATAACTACGATACTAAGGTTACTTTGTTCCACGGC : 327
TrPEPCa3 : CAAGAGGATGTAGTGGCTGCTTGCAATAAGTACGATACTAAGGTTACTTTGTTCCACGGC : 326
TrPEPCa1 : CGTGGAGGCAGTATTGGTCGAGGTGGTGGCCCTACATATCTGGCTATTCAGTCCCAACCA : 479
TrPEPCa2 : CGCGGAGGGAGTATTGGACGTGGCGGAGGCCCAACATATCTGGCTATTCAGTCCCAGCCA : 387
TrPEPCa3 : CGCGGAGGGAGTATTGGACGTGGCGGAGGCCCAACATATCTGGCTATTCAGTCCCAGCCA : 386
TrPEPCa1 : CCTGGGTCTGTGATGGGAACACTTCGGTCTACTGAGCAGGGAGAAATGGTAGAGGCCAAC : 539
TrPEPCa2 : CCTGGCTCTGTGATGGGAACCCTTCGGTCAACTGAGCAGGGACAGATGGTGCAGGCCGAC : 447
TrPEPCa3 : CCTGGCTCTGTGATGGGAACCCTTCGGTCAACTGAGCAGGGAGAGATGGTGCAGGCCGAC : 446
TrPEPCa1 : TTTGCGTTACCACAGAGATACTGTTACACAACTTGANN------------------------ : 576
TrPEPCa2 : TTTGCGTTCCCACAGACAGCAGTTAGACAACTTGAAATATACACAACAGCTGTGCTACTT : 507
TrPEPCa3 : TTTGCGTTCCCACAGACAGCAGTTAGACAACTTGAAATATACACAACAGCTGTGCTACTT : 506

**FIGURE 18**

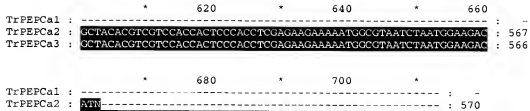


**FIGURE 18 (cont.)**

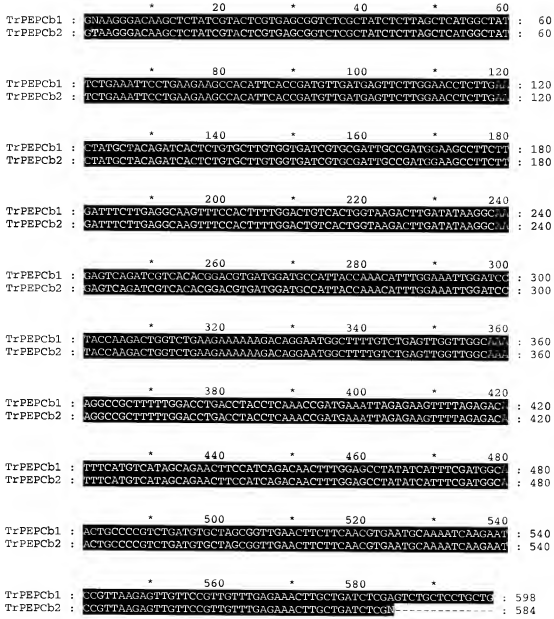


**FIGURE 19**
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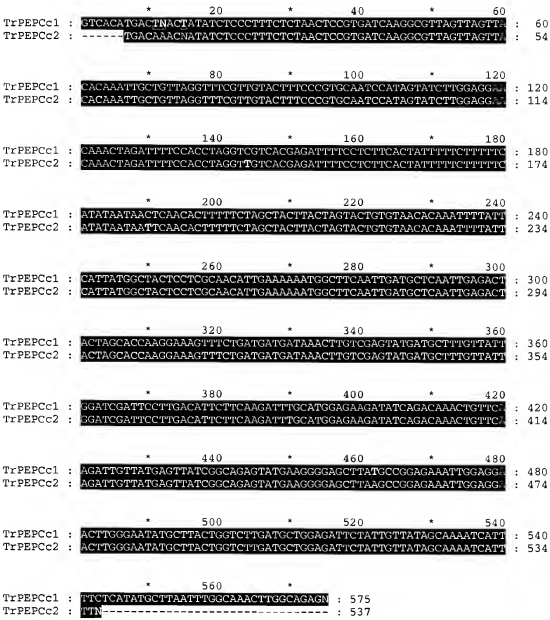


**FIGURE 20**
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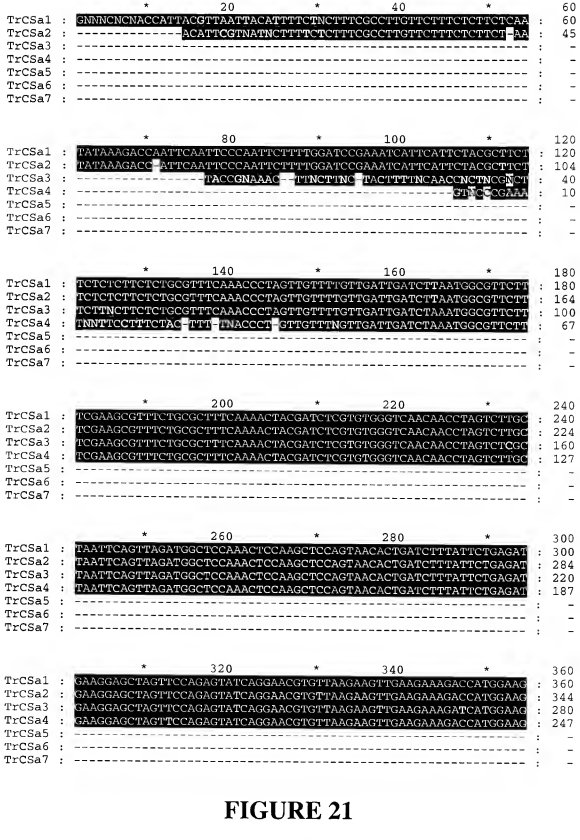



**FIGURE 21**

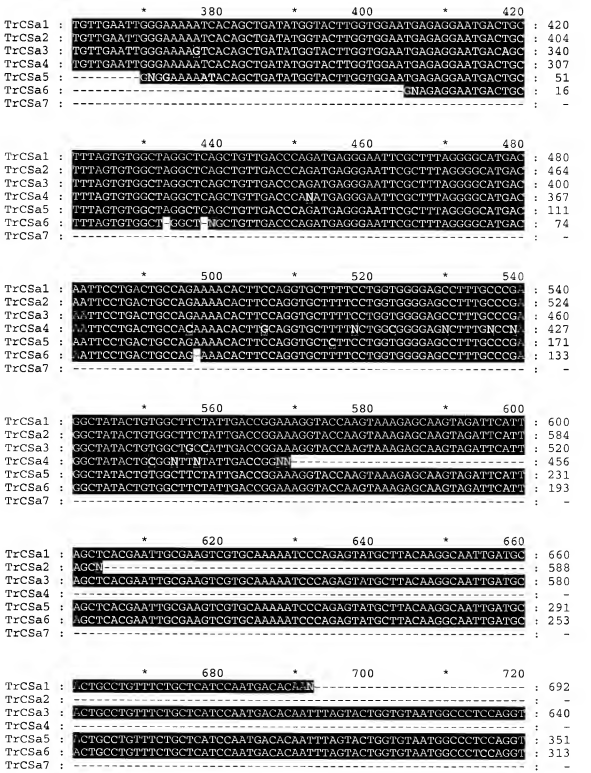


**FIGURE 21 (cont.)**

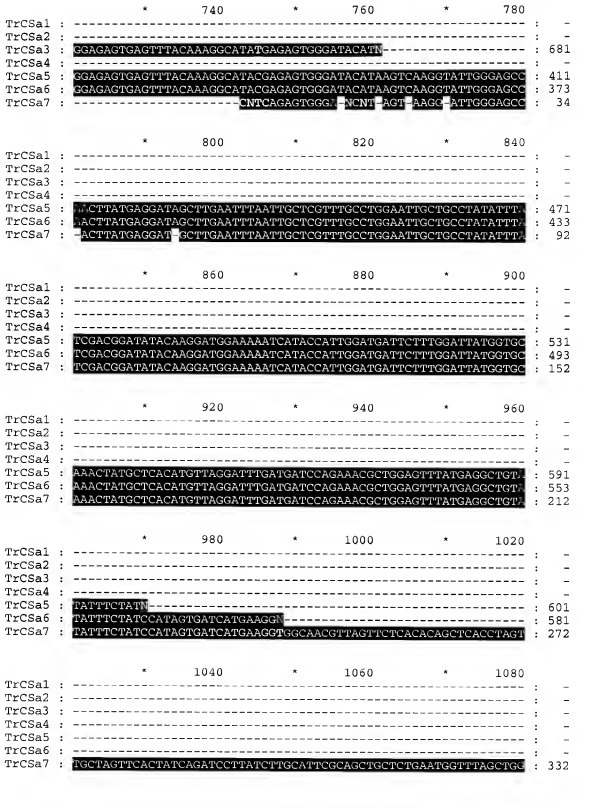



**FIGURE 21 (cont.)**

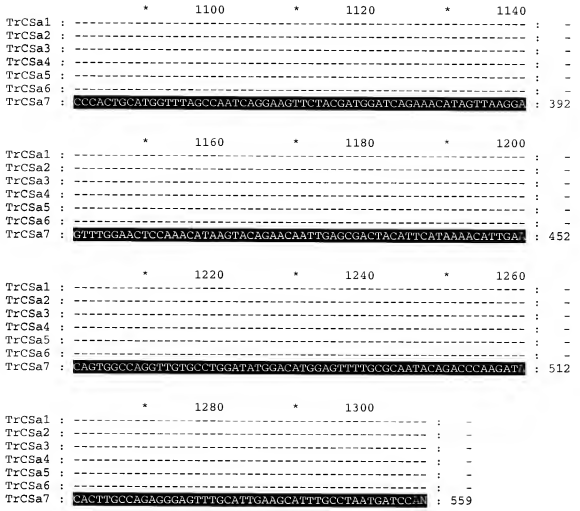



**FIGURE 21 (cont.)**

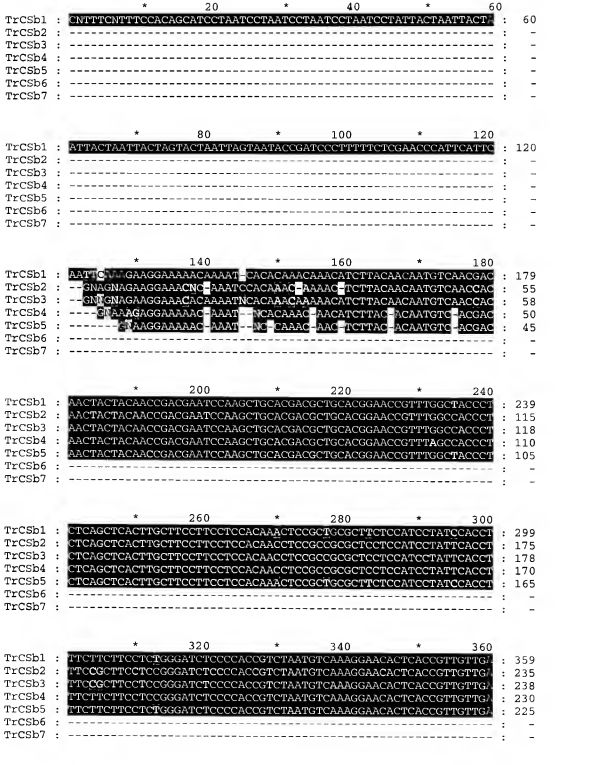

TrCSb1 : CNTTTCNTTTCCACAGCATCCTAATCCTAATCCTAATCCTAATCCTATTACTAATTACTA : 60
TrCSb2 : ---------- : -
TrCSb3 : ---------- : -
TrCSb4 : ---------- : -
TrCSb5 : ---------- : -
TrCSb6 : ---------- : -
TrCSb7 : ---------- : -
TrCSb1 : ATTACTAATTACTAGTACTAATTAGTAATACCGATCCCTTTTTCTCGAACCCATTCATTC : 120
TrCSb2 : ---------- : -
TrCSb3 : ---------- : -
TrCSb4 : ---------- : -
TrCSb5 : ---------- : -
TrCSb6 : ---------- : -
TrCSb7 : ---------- : -
TrCSb1 : AATTCNNNGAAGGAAAAACAAAATNNCACAAACAAACATCTTACAACAATGTCAACGAC : 179
TrCSb2 : --GNAGNAGAAGGAAACNCAAATCCACAAACAAAACATCTTACAACAATGTCAACGAC : 55
TrCSb3 : --GNTGNAGAAGGAAACNCAAAATNCACAAACAAAAACATCTTACAACAATGTCAACGAC : 58
TrCSb4 : ----GNAAAGAGGAAAAACNAAATNNCACAAACNAACATCTTACNACAATGTCNACGAC : 50
TrCSb5 : ------GNAAGGAAAAACNAAATNNCNACAAACNAACATCTTACNACAATGTCNACGAC : 45
TrCSb6 : ---------- : -
TrCSb7 : ---------- : -
TrCSb1 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCTACCCT : 239
TrCSb2 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT : 115
TrCSb3 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT : 118
TrCSb4 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTAGCCACCCT : 110
TrCSb5 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCTACCCT : 105
TrCSb6 : ---------- : -
TrCSb7 : ---------- : -
TrCSb1 : CTCAGCTCACTTGCTTCCTTCCTCCACAAACTCCGCTGCGCTTCTCCATCCTATCCACCT : 299
TrCSb2 : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT : 175
TrCSb3 : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT : 178
TrCSb4 : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT : 170
TrCSb5 : CTCAGCTCACTTGCTTCCTTCCTCCACAAACTCCGCTGCGCTTCTCCATCCTATCCACCT : 165
TrCSb6 : ---------- : -
TrCSb7 : ---------- : -
TrCSb1 : TTCTTCTTCCTCTGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 359
TrCSb2 : TTCCGCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 235
TrCSb3 : TTCCGCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 238
TrCSb4 : TTCTTCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 230
TrCSb5 : TTCTTCTTCCTCTGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 225
TrCSb6 : ---------- : -
TrCSb7 : ---------- : -

**FIGURE 22**

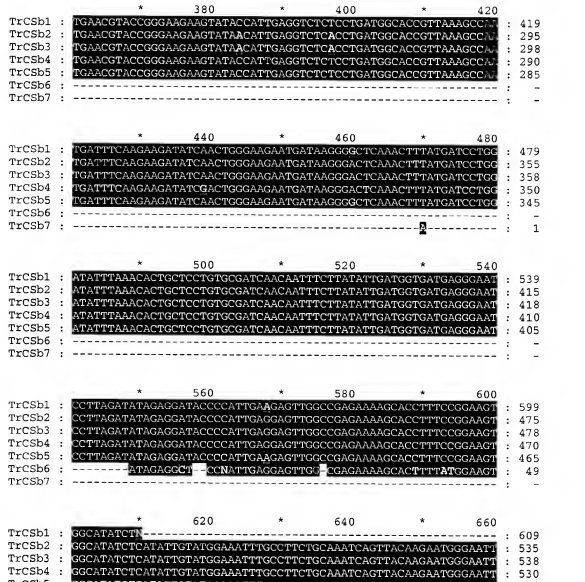



**FIGURE 22 (cont.)**

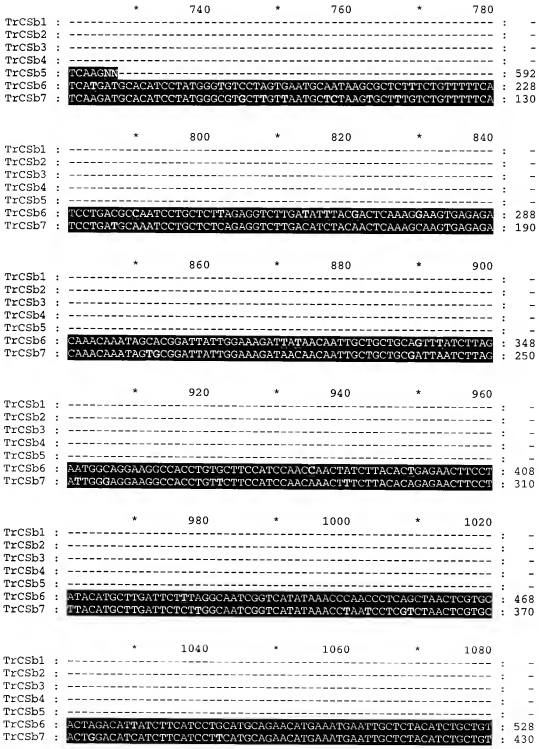



**FIGURE 22 (cont.)**

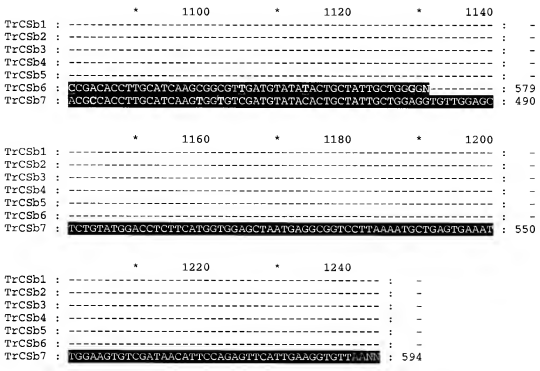
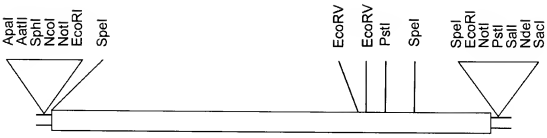



**FIGURE 22 (cont.)**




**TrMDH**

**FIGURE 23**
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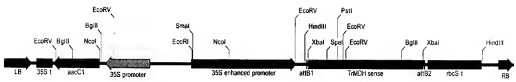
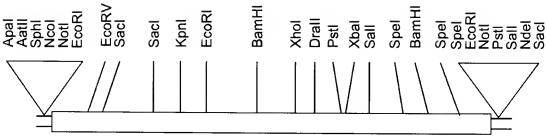



pPZP221:TrMDH sense

**FIGURE 24**




**TrPEPC**

**FIGURE 25**
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pPZP221:TrPEPC sense

**FIGURE 26**
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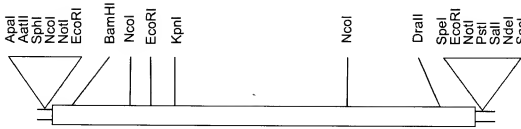


TrCSa

**FIGURE 27**
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pPZP221:TrCSa sense

**FIGURE 28**
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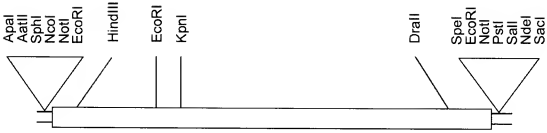


**TrCSb**

**FIGURE 29**
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pPZP221:TrCSb sense

**FIGURE 30**
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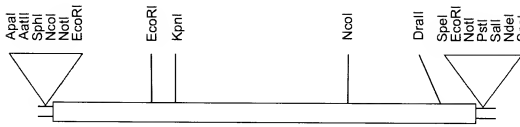


TrCSd

**FIGURE 31**
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pPZP221:TrCSd sense

**FIGURE 32**
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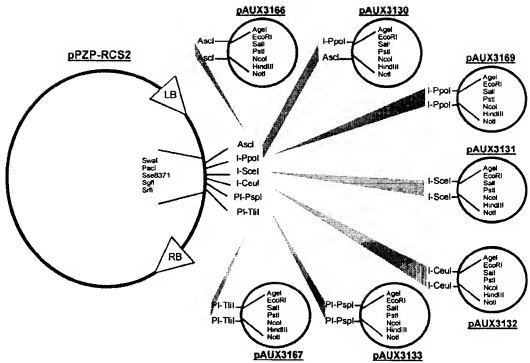


**FIGURE 33**
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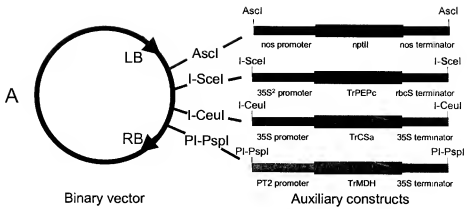



**FIGURE 34**
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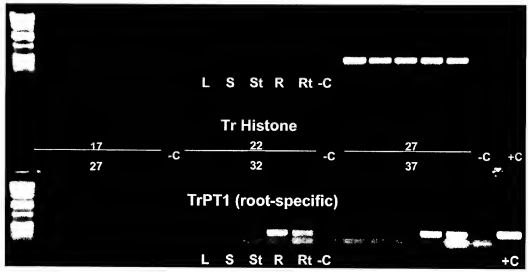
A




B

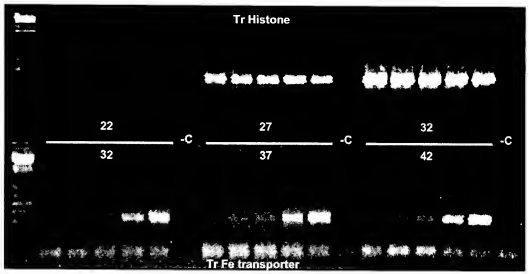



**FIGURE 35**
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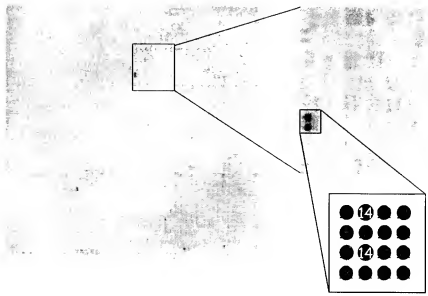
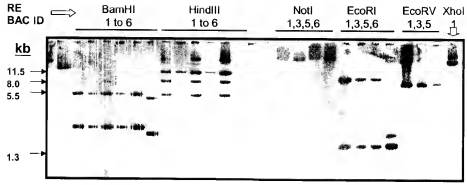
A




B




C

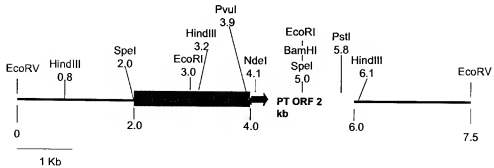



**FIGURE 36**
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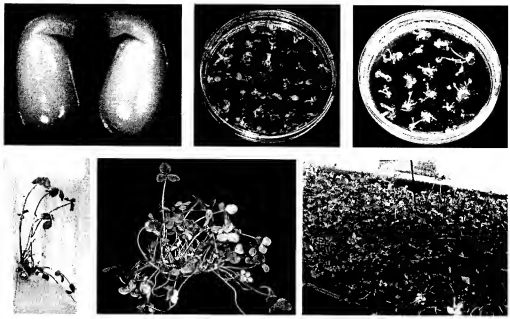

**FIGURE 37**
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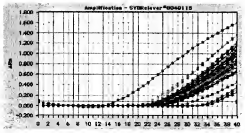
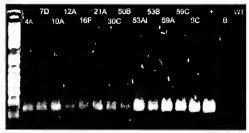
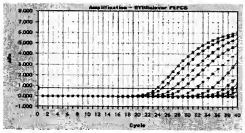


QPCR plots

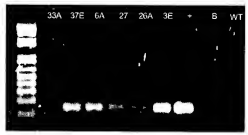



QPCR Result

**FIGURE 38**



QPCR plots




QPCR Result

**FIGURE 39**
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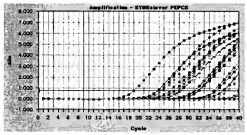
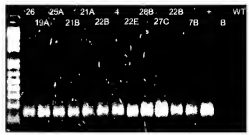


QPCR plots




QPCR Result

**FIGURE 40**